

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 11, 2002, 09:26:45 ; Search time 66.82 Seconds

(without alignments)
3769,900 Million cell updates/sec

Title: US-09-528-031-2

Perfect score: 7308

Sequence: 1 MKDIDGKEIIRPGYRSV.....DSSRFYAMFAENKAVK 1437

Scoring table:

BLOSUM62

Searched: 528882 seqs, 175299045 residues

Total number of hits satisfying chosen parameters: 528882

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7297	99.8	1437	US-10-162-012-38	Sequence 38, Appl
2	7293	99.8	1437	US-09-647-140A-4	Sequence 4, Appl
3	7293	99.8	1437	US-10-154-452-2	Sequence 2, Appl
4	7285	99.7	1437	US-60-389-987-563	Sequence 563, App
5	6674	91.3	1325	US-10-154-452-6	Sequence 6, Appl
6	2664.5	36.4	1382	US-10-087-782A-31	Sequence 31, Appl
7	2540.5	34.8	1360	US-10-162-012-34	Sequence 34, Appl
8	2049.5	28.0	1325	US-09-647-140A-2	Sequence 2, Appl
9	2034.5	27.8	1388	US-60-389-987-1718	Sequence 1718, Ap
10	2023.5	27.7	1510	US-09-935-625-2657	Sequence 2657, A
11	2023.5	27.7	1529	US-09-935-625-26956	Sequence 26956, A
12	2023.5	27.7	1622	US-09-935-625-26955	Sequence 26955, A
13	2013.5	27.6	1510	US-09-935-625-26574	Sequence 26574, A
14	2013.5	27.6	1529	US-09-935-625-26573	Sequence 26573, A
15	2013.5	27.6	1622	US-09-935-625-26572	Sequence 26572, A
16	1992	27.3	1499	US-09-935-625-3013	Sequence 3013, Ap
17	1992	27.3	1499	US-09-935-625-25379	Sequence 25379, A
18	1992	27.3	1530	US-09-935-625-3012	Sequence 3012, Ap
19	1992	27.3	1530	US-09-935-625-25378	Sequence 25378, A
20	1992	27.3	1623	US-09-935-625-3011	Sequence 3011, Ap
21	1992	27.3	1623	US-09-935-625-25377	Sequence 25377, A
22	1988	27.2	1507	US-09-935-625-3328	Sequence 3328, Ap
23	1988	27.2	1507	US-09-935-625-26043	Sequence 26043, A
24	1988	27.2	1538	US-09-935-625-3327	Sequence 3327, Ap
25	1988	27.2	1538	US-09-935-625-26042	Sequence 26042, A
26	1988	27.2	1631	US-09-935-625-3326	Sequence 3326, Ap

ALIGNMENTS

27	1988	27.2	1631	5	US-09-935-625-26041	Sequence 26041, A
28	1984.5	27.1	1515	7	US-60-360-039-6697	Sequence 6697, Ap
29	1983.5	27.1	1515	7	US-60-360-039-1637	Sequence 1637, Ap
30	1941	26.6	1527	5	US-09-647-140A-6	Sequence 6, Appl
31	1923	26.3	1581	6	US-10-179-131-6804	Sequence 6804, Ap
32	1897	26.0	1573	7	US-60-360-039-6867	Sequence 6867, Ap
33	1897	26.0	1573	7	US-60-360-039-6868	Sequence 6868, Ap
34	1896.5	26.0	1508	7	US-60-360-039-4104	Sequence 4104, Ap
35	1874.5	25.6	1444	7	US-60-360-039-2241	Sequence 2241, Ap
36	1828	25.0	1355	5	US-09-935-625-7277	Sequence 7277, Ap
37	1828	25.0	1355	5	US-09-935-625-16233	Sequence 16233, Ap
38	1819.5	24.9	1516	5	US-09-935-625-5376	Sequence 5376, Ap
39	1819.5	24.9	1516	5	US-09-935-625-8196	Sequence 8196, Ap
40	1819.5	24.9	1516	5	US-09-935-625-25430	Sequence 25430, A
41	1819.5	24.9	1516	5	US-09-935-625-5377	Sequence 5377, Ap
42	1806	24.7	1251	5	US-09-935-625-8197	Sequence 8197, Ap
43	1806	24.7	1251	5	US-09-935-625-20410	Sequence 20410, A
44	1806	24.7	1251	5	US-09-935-625-25431	Sequence 25431, A
45	1806	24.7	1251	5	US-09-935-625-25431	Sequence 25431, A

RESULT 1
US-10-162-012-38
Sequence 38, Application US/10162012
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
FILE REFERENCE: 10448-190001
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US/10/162,012
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: US 60/209,845
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: US 09/875,321
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: PCT/US01/18340
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,257
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 09/875,423
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/US01/18398
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,238
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 09/875,363
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/US01/18247
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/227,068
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 09/928,530
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: PCT/US01/25475
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 09/934,421
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/US01/26096
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/279,281
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 10/109,029
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: PCT/US02/09728
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: US (not assigned)
 ; PRIOR FILING DATE: 2002-05-13
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 1437
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-162-012-38

Query Match 99.8%; Score 7297; DB 6; Length 1437;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1437; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDIDGKEIIPSPGSRVREERTSGTTHRDEDSKFRRTPLRECODALETAARAGLS 60
 DB 1 MKDIDGKEIIPSPGSRVREERTSGTTHRDEDSKFRRTPLRECODALETAARAGLS 60
 QY 61 LDASHMSOLILDEHPKCKYHGLSALKPRTTCKHQHPVDNAGLFSCMTFSWLSLAR 120
 DB 61 LDASHMSOLILDEHPKCKYHGLSALKPRTTCKHQHPVDNAGLFSCMTFSWLSLAR 120
 QY 121 VAHKKELSMEDVWSLSKSHSSDVNCRRLERLMOEELNEVGPDAASLRRVWVIFCRRLI 180
 DB 121 VAHKKELSMEDVWSLSKSHSSDVNCRRLERLMOEELNEVGPDAASLRRVWVIFCRRLI 180
 QY 181 LSTVLCMTIOLAGFSGPAFWKHLETOATESNLQYSLLVGLLTETIVRSMLATW 240
 DB 181 LSTVLCMTIOLAGFSGPAFWKHLETOATESNLQYSLLVGLLTETIVRSMLATW 240
 QY 241 ALMYRTGVRGALITLMAFKKILKLNKIKESLIGELINCSNDQORMEFAAVGSLLAG 300
 DB 241 ALMYRTGVRGALITLMAFKKILKLNKIKESLIGELINCSNDQORMEFAAVGSLLAG 300
 QY 301 PVAIIIGMIYNNVILPTGFGSAVFLTFEPAMFASRLTAYFRRCVATDERVOKME 360
 DB 301 PVAIIIGMIYNNVILPTGFGSAVFLTFEPAMFASRLTAYFRRCVATDERVOKME 360
 QY 361 VLTYIKFKMYAWKAFSOSQVKIRREERILKAGYFOSITVGVAPIVVIVIASVTFV 420
 DB 361 VLTYIKFKMYAWKAFSOSQVKIRREERILKAGYFOSITVGVAPIVVIVIASVTFV 420
 QY 421 HMTLGFDTLAAQAFVYVYVNSMTFALKVTPESVKSLSSEASVANDREKSLFMEEVMIK 480
 DB 421 HMTLGFDTLAAQAFVYVYVNSMTFALKVTPESVKSLSSEASVANDREKSLFMEEVMIK 480
 QY 481 NKRPASHIKEMKNATLAMSSSHSSIONSPLKPKMKKORASRGKKEKVRQLOPTEHOA 540
 DB 481 NKRPASHIKEMKNATLAMSSSHSSIONSPLKPKMKKORASRGKKEKVRQLOPTEHOA 540
 QY 541 VLAEOGHLILDSDEPSPREEEGKHILGHLRLQRTLSIDLEIOGKLVGICGSVSG 600
 DB 541 VLAEOGHLILDSDEPSPREEEGKHILGHLRLQRTLSIDLEIOGKLVGICGSVSG 600
 QY 601 KTSLSAIIIGOMTLBGSIAISGTFAYVAQOAMILNATLNDNLLFGKEYDEERYNSVLNS 660
 DB 601 KTSLSAIIIGOMTLBGSIAISGTFAYVAQOAMILNATLNDNLLFGKEYDEERYNSVLNS 660
 QY 661 CCLRPPLATIPSSDLTEIGRGANLSGGQORISLARALSDSISYLLDDPLSALDAHVG 720
 DB 661 CCLRPPLATIPSSDLTEIGRGANLSGGQORISLARALSDSISYLLDDPLSALDAHVG 720
 QY 721 NHTFNSAIRKHLKSKTVLFTVTHOLOYLVDCEVIFMKEGCITFERTHEELMNLNGDATTI 780
 DB 721 NHTFNSAIRKHLKSKTVLFTVTHOLOYLVDCEVIFMKEGCITFERTHEELMNLNGDATTI 780
 QY 781 FNNLLIGETPPVINSKKESSQOKSODKGPRTGSIKKEKAVPEEGQLVLEEGGGS 840
 DB 781 FNNLLIGETPPVINSKKESSQOKSODKGPRTGSIKKEKAVPEEGQLVLEEGGGS 840
 QY 841 VPMSSVGYVIOAGGPLAFVYALFMLANGSAFTWMLSVYIKOSGNTVYTRGNETS 900
 DB 841 VPMSSVGYVIOAGGPLAFVYALFMLANGSAFTWMLSVYIKOSGNTVYTRGNETS 900

DB 841 VPMSSVGYVIOAGGPLAFVYALFMLANGSAFTWMLSVYIKOSGNTVYTRGNETS 900
 QY 901 VDSMKDNPMHQYVYASITAYLSMAVMYLILKAI RGVVFKGLTRASSRHLDELFRRLRSPM 960
 DB 901 VDSMKDNPMHQYVYASITAYLSMAVMYLILKAI RGVVFKGLTRASSRHLDELFRRLRSPM 960
 QY 961 KFEPTPTGRLNRFSSKDMODEVRLPFOAMFIQNLVLFECYGMATAGFPWFLVAVGP 1020
 DB 961 KFEPTPTGRLNRFSSKDMODEVRLPFOAMFIQNLVLFECYGMATAGFPWFLVAVGP 1020
 QY 1021 LVILFSLHTVSRVLRILKELRLDNIQTOSPLSHITSSIOGLATTHAYNKGOEFLHRQEL 1080
 DB 1021 LVILFSLHTVSRVLRILKELRLDNIQTOSPLSHITSSIOGLATTHAYNKGOEFLHRQEL 1080
 QY 1081 LDDNQAPFFLFTCAMRLAVRLDLISALTITTTGLMIVLMHGOIPPAVAGLAISYAVOLT 1140
 DB 1081 LDDNQAPFFLFTCAMRLAVRLDLISALTITTTGLMIVLMHGOIPPAVAGLAISYAVOLT 1140
 QY 1141 GLFQFTVRLASETEARETSVERINHYIKTSLSEAPARIKKNKAPSPDMPDQEGEVTFENAE 1200
 DB 1141 GLFQFTVRLASETEARETSVERINHYIKTSLSEAPARIKKNKAPSPDMPDQEGEVTFENAE 1200
 QY 1201 RYRENPLVLKXVSFTTKPKREKIGIVRTGSGKSLGMLFRLVELSGCCIKTIDVRI 1260
 DB 1201 RYRENPLVLKXVSFTTKPKREKIGIVRTGSGKSLGMLFRLVELSGCCIKTIDVRI 1260
 QY 1261 IGLADLSKLSIIPQEPVLSGTVRSNLDPEFNOYTEDQIINDALERTHMKECIAQLPLKLE 1320
 DB 1261 IGLADLSKLSIIPQEPVLSGTVRSNLDPEFNOYTEDQIINDALERTHMKECIAQLPLKLE 1320
 QY 1321 SEWENGDNFSVGEROLLCTARALLRCKIILIDEATAAMDTELDLIOETIREAFADCT 1380
 DB 1321 SEWENGDNFSVGEROLLCTARALLRCKIILIDEATAAMDTELDLIOETIREAFADCT 1380
 QY 1381 MLTIAHRLHTVLGSDRIMVLAOGVVEFDTPSVLLSDSSRFYAMFAAENKVAVK 1437
 DB 1381 MLTIAHRLHTVLGSDRIMVLAOGVVEFDTPSVLLSDSSRFYAMFAAENKVAVK 1437

RESULT 2
 US-09-647-140A-4
 ; Sequence 4 Application US/09647140A
 ; GENERAL INFORMATION:
 ; APPLICANT: Fox Chase Cancer Center
 ; APPLICANT: Kruh, Gary D.
 ; APPLICANT: Lee, Kun
 ; APPLICANT: Belinsky, Martin G.
 ; APPLICANT: Bain, Lisa J.
 ; TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
 ; FILE REFERENCE: FCCC 98-02
 ; CURRENT APPLICATION NUMBER: US/09/647,140A
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: PCT/US99/06644
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 60/079,759
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/095,153
 ; PRIOR FILING DATE: 1998-08-03
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 1437
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-647-140A-4

Query Match 99.8%; Score 7293; DB 5; Length 1437;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1437; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MKDIDGKEYIIPSPGRSVRETSSTGTHRDREDSKFRTRPLECODALETAARAGLS 60
Oy 61 LDASHMSQRLIDEDEHPKGYHHGSLALKPRTTCKHOHPVDNAGLFSCWTFMSLSLAR 120
Db 61 LDASHMSQRLIDEDEHPKGYHHGSLALKPRTTCKHOHPVDNAGLFSCWTFMSLSLAR 120
Oy 121 VAHKKGELMEDVWSLSKHESSDVNCRRLERLMOEELNEVGPDAASLRVVMJFCRTRL 180
Db 121 VAHKKGELMEDVWSLSKHESSDVNCRRLERLMOEELNEVGPDAASLRVVMJFCRTRL 180
Oy 181 LSVICMINTOLAGFSGPAPMVNHLLEYTOATESNLQYSLVLVGLLTETIVRSMSLATM 240
Db 181 LSVICMINTOLAGFSGPAPMVNHLLEYTOATESNLQYSLVLVGLLTETIVRSMSLATM 240
Oy 241 ALNRYTVRLRGAILTMAFKKILKLNKEKSLGELINICSDNGOMFEAAVAGSLAAG 300
Db 241 ALNRYTVRLRGAILTMAFKKILKLNKEKSLGELINICSDNGOMFEAAVAGSLAAG 300
Oy 301 PVVALIGMITYNYIILGPTGFLGSAVFILFYPAAMFASRLTAFFRRKCVATDERVOKME 360
Db 301 PVVALIGMITYNYIILGPTGFLGSAVFILFYPAAMFASRLTAFFRRKCVATDERVOKME 360
Oy 361 VLTYYIKFKIMYAWKAFSGSVOKIREERRILEKAGYFOSITVGAIVVIAVVSFV 420
Db 361 VLTYYIKFKIMYAWKAFSGSVOKIREERRILEKAGYFOSITVGAIVVIAVVSFV 420
Oy 421 HHTLGFDLTAQAQFVVVYVFNMTFALKTPFSVKSLSASAVADRFKSLFMEEVHMK 480
Db 421 HHTLGFDLTAQAQFVVVYVFNMTFALKTPFSVKSLSASAVADRFKSLFMEEVHMK 480
Oy 481 NKPPASPHIKIEKNKNTIANDSSHSSIONSPLTPPKMKKRRASRGKEVROLQRTHOA 540
Db 481 NKPPASPHIKIEKNKNTIANDSSHSSIONSPLTPPKMKKRRASRGKEVROLQRTHOA 540
Oy 541 VLAEOGHLLDSDERPSPREEEGKHILGHLRLQRTLSIDLEIOEGKLVIGCSVSGS 600
Db 541 VLAEOGHLLDSDERPSPREEEGKHILGHLRLQRTLSIDLEIOEGKLVIGCSVSGS 600
Oy 601 KTSLSAISAILGOMTLEGSIAISGTAYVAQOAMILNATLRDNLFEKEDEERYNSVLNS 660
Db 601 KTSLSAISAILGOMTLEGSIAISGTAYVAQOAMILNATLRDNLFEKEDEERYNSVLNS 660
Oy 661 CCLRPDLALPSSDLTEIERGANLSCGORRISLARALYSRSTIYLLDPLSALDAHVG 720
Db 661 CCLRPDLALPSSDLTEIERGANLSCGORRISLARALYSRSTIYLLDPLSALDAHVG 720
Oy 721 NHIFNSAIRKHLKSKTVLFTVHQLOYLVDCDEVIFMKKECITERGTHEELMNLNGDYAT 780
Db 721 NHIFNSAIRKHLKSKTVLFTVHQLOYLVDCDEVIFMKKECITERGTHEELMNLNGDYAT 780
Oy 781 FNNLLGEPPEVEINSKKTSGSKSODKGRKTSIKKEKAVKPEEGOLVOLEEGGGS 840
Db 781 FNNLLGEPPEVEINSKKTSGSKSODKGRKTSIKKEKAVKPEEGOLVOLEEGGGS 840
Oy 841 VMSVYGVYIOAAGPLAVLTMALFMLNVGSTASTMWSWIKOGSGNTVTRGENS 900
Db 841 VMSVYGVYIOAAGPLAVLTMALFMLNVGSTASTMWSWIKOGSGNTVTRGENS 900
Oy 901 VSDSKNDPNHMOYASISALMAVMLILKAIKGVVFKTGLASSRLHJELFRILSRSM 960
Db 901 VSDSKNDPNHMOYASISALMAVMLILKAIKGVVFKTGLASSRLHJELFRILSRSM 960
Oy 961 KFFDTPPGRIILNRSKMDDEVNRLPFOAEFIONVILVFCVGMIAVFPWFVAVGP 1020
Db 961 KFFDTPPGRIILNRSKMDDEVNRLPFOAEFIONVILVFCVGMIAVFPWFVAVGP 1020
Oy 1021 LVTLSSVLIYSRVILRELKRDNTOSPELSTISSIOGLATIAVYNGOEELHAYOEL 1080
Db 1021 LVTLSSVLIYSRVILRELKRDNTOSPELSTISSIOGLATIAVYNGOEELHAYOEL 1080
Oy 1081 LDDNOAPFELFTCAMRWLAVRLDLISALITTTGLMIVLMHGOIPPAVAGLAISYAVOLT 1140

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Db 1081 LDDNOAPFELFTCAMRWLAVRLDLISALITTTGLMIVLMHGOIPPAVAGLAISYAVOLT 1140
Oy 1141 GLFOFTVRLASERAEFTSVERTNHITKLSLEAPARINKKASPDWQEGEFTFENAEK 1200
Db 1141 GLFOFTVRLASERAEFTSVERTNHITKLSLEAPARINKKASPDWQEGEFTFENAEK 1200
Oy 1201 RYRENPLVLKVSFTIKRKEKIGIVRGSGSSGMLFLRVLESGCCIKIDGRISD 1260
Db 1201 RYRENPLVLKVSFTIKRKEKIGIVRGSGSSGMLFLRVLESGCCIKIDGRISD 1260
Oy 1261 IGLADRSKLSIIPBVLFSGTVRSNLDPEFNOYTEDQIWDALERTHMECIALPLKLE 1320
Db 1261 IGLADRSKLSIIPBVLFSGTVRSNLDPEFNOYTEDQIWDALERTHMECIALPLKLE 1320
Oy 1321 SEVMENGDNFSVGEROLLCTARALLRCKILLIDEATAMDPETDILIOETIEAFADCT 1380
Db 1321 SEVMENGDNFSVGEROLLCTARALLRCKILLIDEATAMDPETDILIOETIEAFADCT 1380
Oy 1381 MLTIAHRLHTVLGSDRINYLAQGOVEFDPVSVLNSDSRFYAMFPAENKVAVG 1437
Db 1381 MLTIAHRLHTVLGSDRINYLAQGOVEFDPVSVLNSDSRFYAMFPAENKVAVG 1437

```

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RESULT 3
US-10-154-452-2
; Sequence 2, Application us/10154452
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Roy, Josee
; TITLE OF INVENTION: INCREASED FUNCTIONAL ACTIVITY AND/OR
; TITLE OF INVENTION: EXPRESSION OF ABC TRANSPORTERS PROTECTS AGAINST THE LOSS OF
; TITLE OF INVENTION: DOPAMINE NEURONS ASSOCIATED WITH PARKINSON'S DISEASE
; FILE REFERENCE: 100103.420
; CURRENT APPLICATION NUMBER: US/10/154.452
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1437
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-452-2

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Query Match          99.8%; Score 7293; DB 6; Length 1437;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1434; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 MKDIDGKEYIIPSPGRSVRETSSTGTHRDREDSKFRTRPLECODALETAARAGLS 60
Db 1 MKDIDGKEYIIPSPGRSVRETSSTGTHRDREDSKFRTRPLECODALETAARAGLS 60
Oy 61 LDASHMSQRLIDEDEHPKGYHHGSLALKPRTTCKHOHPVDNAGLFSCWTFMSLSLAR 120
Db 61 LDASHMSQRLIDEDEHPKGYHHGSLALKPRTTCKHOHPVDNAGLFSCWTFMSLSLAR 120
Oy 121 VAHKKGELMEDVWSLSKHESSDVNCRRLERLMOEELNEVGPDAASLRVVMJFCRTRL 180
Db 121 VAHKKGELMEDVWSLSKHESSDVNCRRLERLMOEELNEVGPDAASLRVVMJFCRTRL 180
Oy 181 LSVICMINTOLAGFSGPAPMVNHLLEYTOATESNLQYSLVLVGLLTETIVRSMSLATM 240
Db 181 LSVICMINTOLAGFSGPAPMVNHLLEYTOATESNLQYSLVLVGLLTETIVRSMSLATM 240
Oy 241 ALNRYTVRLRGAILTMAFKKILKLNKEKSLGELINICSDNGOMFEAAVAGSLAAG 300
Db 241 ALNRYTVRLRGAILTMAFKKILKLNKEKSLGELINICSDNGOMFEAAVAGSLAAG 300
Oy 301 PVVALIGMITYNYIILGPTGFLGSAVFILFYPAAMFASRLTAFFRRKCVATDERVOKME 360
Db 301 PVVALIGMITYNYIILGPTGFLGSAVFILFYPAAMFASRLTAFFRRKCVATDERVOKME 360

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QY 361 VLTIFYIKMYANVAKASQVOKIREEERILEKAGYFOSITWGVADIVVIVIASVTFVSV 420
 Db 361 VLTIFYIKMYANVAKASQVOKIREEERILEKAGYFOSITWGVADIVVIVIASVTFVSV 420
 QY 421 HMTLGFDLTAQAFTVTVNSMTFALKVTFVSYSLEASVAVDRKSLFLMEEVMIK 480
 Db 421 HMTLGFDLTAQAFTVTVNSMTFALKVTFVSYSLEASVAVDRKSLFLMEEVMIK 480
 QY 481 NKPSAPHIKEMKNATLAMDSSSHSSIONSPLPKMKKDRASGKKEKYROLORTEHOA 540
 Db 481 NKPSAPHIKEMKNATLAMDSSSHSSIONSPLPKMKKDRASGKKEKYROLORTEHOA 540
 QY 541 VLAQKGHLLDSDERSPEEBEGKHHLGHLRLQRTLHSDLEIOGKLVIGCSYVSG 600
 Db 541 VLAQKGHLLDSDERSPEEBEGKHHLGHLRLQRTLHSDLEIOGKLVIGCSYVSG 600
 QY 601 KTSLSIALIGOMTLBESIAISGTFAYVAOAWMLNATLNLFGKEYDEERYNSVLNS 660
 Db 601 KTSLSIALIGOMTLBESIAISGTFAYVAOAWMLNATLNLFGKEYDEERYNSVLNS 660
 QY 661 CCLRPDLALPSSDLTEIGERGANTSGGQORISLARALYSDSISYLLDDPLSALDAHV 720
 Db 661 CCLRPDLALPSSDLTEIGERGANTSGGQORISLARALYSDSISYLLDDPLSALDAHV 720
 QY 721 NHIFNSAIRKHLKSKYVLYVTHOLOYLVDCEVIFPKKESCTTERGHEELMNLGDIAT 780
 Db 721 NHIFNSAIRKHLKSKYVLYVTHOLOYLVDCEVIFPKKESCTTERGHEELMNLGDIAT 780
 QY 781 FNNLLGEPPEVPEINSKKEYSOGSKODKPGTGSIKKREKAVPEEGOLVOLEEKOGS 840
 Db 781 FNNLLGEPPEVPEINSKKEYSOGSKODKPGTGSIKKREKAVPEEGOLVOLEEKOGS 840
 QY 841 VPMVSYGVYIOAAGPLAFLVIALFMLNNGSTAFSTWMLSYWIKOSGNTVYRGNETS 900
 Db 841 VPMVSYGVYIOAAGPLAFLVIALFMLNNGSTAFSTWMLSYWIKOSGNTVYRGNETS 900
 QY 901 VPSMKDNPMOYIYASIALSMAVMLLKAIKGVYVFKGLRASSRLMDELFRILRSPM 960
 Db 901 VPSMKDNPMOYIYASIALSMAVMLLKAIKGVYVFKGLRASSRLMDELFRILRSPM 960
 QY 961 KFPDTPTRGRLNRFESKDMDEVNRLPFOAEMFIONVILVFECVMAGVFPMLVAVGP 1020
 Db 961 KFPDTPTRGRLNRFESKDMDEVNRLPFOAEMFIONVILVFECVMAGVFPMLVAVGP 1020
 QY 1021 LVTLFVLAHVSRLNRELKRLDNTQSPLSHITSSIOGLATIHAVNKGOEFLHRYOEL 1080
 Db 1021 LVTLFVLAHVSRLNRELKRLDNTQSPLSHITSSIOGLATIHAVNKGOEFLHRYOEL 1080
 QY 1081 LDNOAPFELFTCAMRMLAVRLDLISALITTTGMLVLMHGQIPRAYAGLAISYAVOLT 1140
 Db 1081 LDNOAPFELFTCAMRMLAVRLDLISALITTTGMLVLMHGQIPRAYAGLAISYAVOLT 1140
 QY 1141 GLPQFYRLASETEARTSEVERINHYIKTSLSEAPARIKKAPSPDPOBGEVFEENAE 1200
 Db 1141 GLPQFYRLASETEARTSEVERINHYIKTSLSEAPARIKKAPSPDPOBGEVFEENAE 1200
 QY 1201 RYRENPPLVLYKVSFTIKPEKIGIVRTSGSKSLGMAFLRVLVELSGGCIKIDGVARISD 1260
 Db 1201 RYRENPPLVLYKVSFTIKPEKIGIVRTSGSKSLGMAFLRVLVELSGGCIKIDGVARISD 1260
 QY 1261 IGLADLRSKSLIIPQEVYLFSGTVRSNLDPPNOYTEDOIDALERTHMKECIAOLPLKLE 1320
 Db 1261 IGLADLRSKSLIIPQEVYLFSGTVRSNLDPPNOYTEDOIDALERTHMKECIAOLPLKLE 1320
 QY 1321 SEYMENGDNSVGEROLCTARALLRHCKILLIDEAANAADTEFDLLIOETIRAFADCT 1380
 Db 1321 SEYMENGDNSVGEROLCTARALLRHCKILLIDEAANAADTEFDLLIOETIRAFADCT 1380
 QY 1381 MLTIAHRLHTVLSGDRIMVLAQGVVEFDTPSVYLLSNDSSRFYAMFAAENKAVKVG 1437
 Db 1381 MLTIAHRLHTVLSGDRIMVLAQGVVEFDTPSVYLLSNDSSRFYAMFAAENKAVKVG 1437

RESULT 4
 US-60-389-987-563
 ; Sequence 563, Application US/60389987
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Martnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; FILE REFERENCE: 660088.465P2
 ; CURRENT APPLICATION NUMBER: US/60/389,987
 ; CURRENT FILING DATE: 2002-06-17
 ; NUMBER OF SEQ. ID NOS: 3025
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 563
 ; LENGTH: 1437
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-389-987-563

Query Match 99.7%; Score 7285; DB 7; Length 1437;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1433; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MKDIDIKKEYIIPSPGRSVREERTSGTHDRDRDSKFRRTRECODALETARAGLS 60
 Db 1 MKDIDIKKEYIIPSPGRSVREERTSGTHDRDRDSKFRRTRECODALETARAGLS 60
 QY 61 LDASMSQLRLDDEHFKGKYHGLSALKPRTCTCKHQHPVNDAGLSCMTFFSWLSLAR 120
 Db 61 LDASMSQLRLDDEHFKGKYHGLSALKPRTCTCKHQHPVNDAGLSCMTFFSWLSLAR 120
 QY 121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLMOBELNEVGPDAASLRVYVIFCRTL 180
 Db 121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLMOBELNEVGPDAASLRVYVIFCRTL 180
 QY 181 LSTYCLMTOAGSGPAPVWKHLLEYTOAESNLOYSLLVLLLTETIYRMSLALTW 240
 Db 181 LSTYCLMTOAGSGPAPVWKHLLEYTOAESNLOYSLLVLLLTETIYRMSLALTW 240
 QY 241 ALNRTGVRGLGALITLTAFFKTLIKLNKKEKSLGELINICSDNGORMEFAAAGSLLAG 300
 Db 241 ALNRTGVRGLGALITLTAFFKTLIKLNKKEKSLGELINICSDNGORMEFAAAGSLLAG 300
 QY 301 PVVAIIIGMIYVILIGPTGLGSAVFLFYPPAMFPASRLTAYFRKKCAVATDERVQKME 360
 Db 301 PVVAIIIGMIYVILIGPTGLGSAVFLFYPPAMFPASRLTAYFRKKCAVATDERVQKME 360
 QY 361 VLTIFYIKMYANVAKASQVOKIREEERILEKAGYFOSITWGVADIVVIVIASVTFVSV 420
 Db 361 VLTIFYIKMYANVAKASQVOKIREEERILEKAGYFOSITWGVADIVVIVIASVTFVSV 420
 QY 421 HMTLGFDLTAQAFTVTVNSMTFALKVTFVSYSLEASVAVDRKSLFLMEEVMIK 480
 Db 421 HMTLGFDLTAQAFTVTVNSMTFALKVTFVSYSLEASVAVDRKSLFLMEEVMIK 480
 QY 481 NKPSAPHIKEMKNATLAMDSSSHSSIONSPLPKMKKDRASGKKEKYROLORTEHOA 540
 Db 481 NKPSAPHIKEMKNATLAMDSSSHSSIONSPLPKMKKDRASGKKEKYROLORTEHOA 540
 QY 541 VLAQKGHLLDSDERSPEEBEGKHHLGHLRLQRTLHSDLEIOGKLVIGCSYVSG 600
 Db 541 VLAQKGHLLDSDERSPEEBEGKHHLGHLRLQRTLHSDLEIOGKLVIGCSYVSG 600
 QY 601 KTSLSIALIGOMTLBESIAISGTFAYVAOAWMLNATLNLFGKEYDEERYNSVLNS 660
 Db 601 KTSLSIALIGOMTLBESIAISGTFAYVAOAWMLNATLNLFGKEYDEERYNSVLNS 660

QY 661 CCLRPDLALIPSSDLTEIGERGANLSGGORISLARALYSDBRSIYLDDPLSALDAHV 720
DB 661 CCLRPDLALIPSSDLTEIGERGANLSGGORISLARALYSDBRSIYLDDPLSALDAHV 720
QY 721 NHFNSAIRKHLKSKTVLFTVHOLOLYVDCDEVIFPKKSGCITRGHHEELMNGDYATI 780
DB 721 NHFNSAIRKHLKSKTVLFTVHOLOLYVDCDEVIFPKKSGCITRGHHEELMNGDYATI 780
QY 781 FNNLLGEPPEVEINSKKETSQSKSODKPKTGSIKKKAAYKPEEGQVLVEEKGGS 840
DB 781 FNNLLGEPPEVEINSKKETSQSKSODKPKTGSIKKKAAYKPEEGQVLVEEKGGS 840
QY 841 VPMYSYGVYIQAAGGFLAFVIALFMLNNGSTAFSTWMLSYWIKOGSGTWTYRGNETS 900
DB 841 VPMYSYGVYIQAAGGFLAFVIALFMLNNGSTAFSTWMLSYWIKOGSGTWTYRGNETS 900
QY 901 VSDSMKDNPHMOYASIVALSMAVMLILKAIKRGVVEFKGLTRASSRLHDELFRILRSPM 960
DB 901 VSDSMKDNPHMOYASIVALSMAVMLILKAIKRGVVEFKGLTRASSRLHDELFRILRSPM 960
QY 961 KFFDTPPTGRILNRFSGKMDDEVDRLPFOAEMFIQNVILVFCVGMAGVPMFLVAVGP 1020
DB 961 KFFDTPPTGRILNRFSGKMDDEVDRLPFOAEMFIQNVILVFCVGMAGVPMFLVAVGP 1020
QY 1021 LVILFVSLHIVSRVILRELKRLDNITQSPPLSHITSIOGLATIHYNKGQEFLLHRYOEL 1080
DB 1021 LVILFVSLHIVSRVILRELKRLDNITQSPPLSHITSIOGLATIHYNKGQEFLLHRYOEL 1080
QY 1081 LDDNQAPFELFCAMRWLAVRLDLISALITTTGLMIVLMHGOIPPAVAGLAISYAVOLT 1140
DB 1081 LDDNQAPFELFCAMRWLAVRLDLISALITTTGLMIVLMHGOIPPAVAGLAISYAVOLT 1140
QY 1141 GLFOFVRLASERFARFVERINHYIKTSLSEAPARINKKAPSPMPQEGVTEFENAEK 1200
DB 1141 GLFOFVRLASERFARFVERINHYIKTSLSEAPARINKKAPSPMPQEGVTEFENAEK 1200
QY 1201 RRRENPLVLKKVSTFIKREKIGIVRTGSGKSSGLMALFRLVELSGGCIKIDGRISD 1260
DB 1201 RRRENPLVLKKVSTFIKREKIGIVRTGSGKSSGLMALFRLVELSGGCIKIDGRISD 1260
QY 1261 IGLADLRKSLSIIPQEPVLFSGTVRSNLDPFNOYTEDQIWDALERTHMKECIAQLPLKLE 1320
DB 1261 IGLADLRKSLSIIPQEPVLFSGTVRSNLDPFNOYTEDQIWDALERTHMKECIAQLPLKLE 1320
QY 1321 SEWMENGDNFVSGERQLCIARALLRCKLILIDEATAAMDPTDILIOETIREAFADCT 1380
DB 1321 SEWMENGDNFVSGERQLCIARALLRCKLILIDEATAAMDPTDILIOETIREAFADCT 1380
QY 1381 MNTIAHRLATVIGSDRIMVLAOGQVVEFPTPSVLLSNDSSREYAMFAAENKVAAYK 1437
DB 1381 MNTIAHRLATVIGSDRIMVLAOGQVVEFPTPSVLLSNDSSREYAMFAAENKVAAYK 1437

RESULT
US-10-154-452-6
Sequence 6, Application US/10154452
GENERAL INFORMATION:
APPLICANT: Reiner, Peter B.
APPLICANT: Roy, Josee
TITLE OF INVENTION: INCREASED FUNCTIONAL ACTIVITY AND/OR
TITLE OF INVENTION: EXPRESSION OF ABC TRANSPORTERS PROTECTS AGAINST THE LOSS OF
TITLE OF INVENTION: DOPAMINE NEURONS ASSOCIATED WITH PARKINSON'S DISEASE
FILE REFERENCE: 100103.420
CURRENT APPLICATION NUMBER: US/10/154,452
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 1325
TYPE: PRT
ORGANISM: Homo sapiens
US-10-154-452-6

Query Match 91.3%; Score 6674; DB 6; Length 1325;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1309; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKDIDIGKEYIIPSPGYSVRETSSTGTHRDEDSKFRRTPLDECODALETAARAGLS 60
DB 1 MEDIDIGKEYIIPSPGYSVRETSSTGTHRDEDSKFRRTPLDECODALETAARAGLS 60
QY 61 LDASMSOLRLIDEEHPKGYHHGLSALKPIRTTCKQHYPVNDAGLFSCMTFMSLSLAR 120
DB 61 LDASMSOLRLIDEEHPKGYHHGLSALKPIRTTCKQHYPVNDAGLFSCMTFMSLSLAR 120
QY 121 VAHKGELSMEDVWSLSKHESSDVNCRRLERLMOEELNEVGPPAASLRVWVIFCRRRLI 180
DB 121 VAHKGELSMEDVWSLSKHESSDVNCRRLERLMOEELNEVGPPAASLRVWVIFCRRRLI 180
QY 181 LSTVCLMITDLAGFSGPAFWKHLLEYTOATESNLQYSLILVGLLLETVRSMSLATW 240
DB 181 LSTVCLMITDLAGFSGPAFWKHLLEYTOATESNLQYSLILVGLLLETVRSMSLATW 240
QY 241 ALMYRTGVRLGAILTMAFKKILKLNKIKESIGELINICSNDGQRFEEAAVAGSLLAGG 300
DB 241 ALMYRTGVRLGAILTMAFKKILKLNKIKESIGELINICSNDGQRFEEAAVAGSLLAGG 300
QY 301 PVVAILGMITVNTILGPTGFLSAVFLFYPAAMFASRLTAYRRKCVAAATERVOKME 360
DB 301 PVVAILGMITVNTILGPTGFLSAVFLFYPAAMFASRLTAYRRKCVAAATERVOKME 360
QY 361 VLYYIKFIKMYAWKAFSOSVOKIREERILKAGVFOSTITGVAPIVVAIVSYVFEV 420
DB 361 VLYYIKFIKMYAWKAFSOSVOKIREERILKAGVFOSTITGVAPIVVAIVSYVFEV 420
QY 421 HMTLGEDLTAAOFTVTVYFNSMTFALKVTPFSYKSLSEASVAVDRKSLFLEEYAMIK 480
DB 421 HMTLGEDLTAAOFTVTVYFNSMTFALKVTPFSYKSLSEASVAVDRKSLFLEEYAMIK 480
QY 481 NKPASPIKITEMNATLAWSSHSIIONSPLTPKMKKDRASGKKEKROLQREHQA 540
DB 481 NKPASPIKITEMNATLAWSSHSIIONSPLTPKMKKDRASGKKEKROLQREHQA 540
QY 541 VLAEOGHLLDDEDERSPREEGKHIGHLRLQRTLSIDIEIOBGKLVGICGSVSG 600
DB 541 VLAEOGHLLDDEDERSPREEGKHIGHLRLQRTLSIDIEIOBGKLVGICGSVSG 600
QY 601 KTSLSAILGOMTLLEGSIAISCTFAVVAOAMILNATLDRNLLFKEXYDEERYNSVLS 660
DB 601 KTSLSAILGOMTLLEGSIAISCTFAVVAOAMILNATLDRNLLFKEXYDEERYNSVLS 660
QY 661 CCLRPDLALIPSSDLTEIGERGANLSGGORISLARALYSDBRSIYLDDPLSALDAHV 720
DB 661 CCLRPDLALIPSSDLTEIGERGANLSGGORISLARALYSDBRSIYLDDPLSALDAHV 720
QY 721 NHFNSAIRKHLKSKTVLFTVHOLOLYVDCDEVIFPKKSGCITRGHHEELMNGDYATI 780
DB 721 NHFNSAIRKHLKSKTVLFTVHOLOLYVDCDEVIFPKKSGCITRGHHEELMNGDYATI 780
QY 781 FNNLLGEPPEVEINSKKETSQSKSODKPKTGSIKKKAAYKPEEGQVLVEEKGGS 840
DB 781 FNNLLGEPPEVEINSKKETSQSKSODKPKTGSIKKKAAYKPEEGQVLVEEKGGS 840
QY 841 VPMYSYGVYIQAAGGFLAFVIALFMLNNGSTAFSTWMLSYWIKOGSGTWTYRGNETS 900
DB 841 VPMYSYGVYIQAAGGFLAFVIALFMLNNGSTAFSTWMLSYWIKOGSGTWTYRGNETS 900
QY 901 VSDSMKDNPHMOYASIVALSMAVMLILKAIKRGVVEFKGLTRASSRLHDELFRILRSPM 960
DB 901 VSDSMKDNPHMOYASIVALSMAVMLILKAIKRGVVEFKGLTRASSRLHDELFRILRSPM 960
QY 961 KFFDTPPTGRILNRFSGKMDDEVDRLPFOAEMFIQNVILVFCVGMAGVPMFLVAVGP 1020
DB 961 KFFDTPPTGRILNRFSGKMDDEVDRLPFOAEMFIQNVILVFCVGMAGVPMFLVAVGP 1020

QY 1021 LVILFSLVLIHSKVLRELKRLDNITQSPPLSHITSSIOGLATIHAYNKGQEFLLHRYOEL 1080
DB 1021 LVILFSLVLIHSKVLRELKRLDNITQSPPLSHITSSIOGLATIHAYNKGQEFLLHRYOEL 1080
QY 1081 LDNOAPFFLETCAMRLAVRLDLISALTITTTGMLVLMHGQIPRAYAGLAISYAOULT 1140
DB 1081 LDNOAPFFLETCAMRLAVRLDLISALTITTTGMLVLMHGQIPRAYAGLAISYAOULT 1140
QY 1141 GLFOFVRLASETEARTSVTERINHYIKTSLLEAPARIKKASPDPPOGEVTFEENAE 1200
DB 1141 GLFOFVRLASETEARTSVTERINHYIKTSLLEAPARIKKASPDPPOGEVTFEENAE 1200
QY 1201 RYRENNPLVLYKVSFTIKPREKIGIVGRTSGSKSSIGMALFRLVELSGGCIKIDGVRISD 1260
DB 1201 RYRENNPLVLYKVSFTIKPREKIGIVGRTSGSKSSIGMALFRLVELSGGCIKIDGVRISD 1260
QY 1261 IGLADLRKSLIIPQEPVLFSGTVRSNLDPPNOYTEDQIWDALERTHMKECI 1312
DB 1261 IGLADLRKSLIIPQEPVLFSGTVRSNLDPPNOYTEDQIWDALERTHMKECI 1312

RESULT 6

US-10-087-782A-31
Sequence 31, Application US/10087782A
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMA SA
APPLICANT: US GOVERNMENT OF THE UNITED STATES
TITLE OF INVENTION: NUCLEIC ACID OF THE HUMAN ABC11 GENE, VECTORS
TITLE OF INVENTION: CONTAINING SUCH NUCLEIC ACID, AND USES THEREOF
FILE REFERENCE: ABC11 GENE
CURRENT APPLICATION NUMBER: US/10/087, 782A
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/272, 757
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 31
LENGTH: 1382
TYPE: PRN
ORGANISM: Homo sapiens
US-10-087-782A-31

Query Match 36.4%; Score 2663.5; DB 6; Length 1382;
Best Local Similarity 40.8%; Pred. No. 1.9e-189;
Matches 556; Conservative 258; Mismatches 501; Indels 49; Gaps 8;

QY 77 PKGKTHHGLSALKPRTTCKH--QHPVDNAGLSCMTFSWLSLARVAHKKGELMEDVW 134
DB 60 PMGKYDALRTMIPFRKPPRPAPQPLDNAGLSTYLVSWLTP--MTQSLRSRIDENTIP 118
QY 135 SLKHHSSDVNCRLELMOEELNEVGPDAASLRVWICRPTLLISYICMTTOLAGF 194
DB 119 PLSHHDSDKNVOKLRLMEEVSRGIEKASVLLVMRFQRTKLIDALGICFCIASV 178
QY 195 SGPAFWKHLLEYQATENSLOYSLILVGLILTEIYRSALATWMLNTYGYRLGAI 254
DB 179 LGLPILILPKLLEKSEGLGVNVHVGICFALFLSECVKSLSFSSSWIINQRTAIRFAAV 238
QY 255 LTMAFKILKLNKIKESLIGELINCSNDGORMEAAVSLAGGPPVAILGMIYVIT 314
DB 239 SSPAFELKIOFKSVIHTITSEAIISFTGDVNVLEPGVCYGLVITCASIVICISSYFI 298
QY 315 LGPTGFLGSAVILIFYANMFASRLTAYFRKCAATADERQKNEVLYTIKFKTAMAV 374
DB 299 IGYTAFALICYLVLVPLAVFMTMAVKAQHHSSEVSDQRTVSEVLTCTKILKMTWE 358
QY 375 KASOSQOKIREBERLLEKAGYFOSITGVAPIVVIVIASVTFQSHMTLGFDTLTAQAF 434
DB 359 KPPAKITIEDLRKREKRLLEKCGVQSLSTITFLIIPVATAVWVLIHTSLKLTATSMAP 418
QY 435 TVYTVFNSMTFALKVTPFPVSLSSEASVAVDRKSLFLMEEVHMKNNKPASPPIKIEKN 494

DB 419 SMLASLMLRLSYEFVIAVAKGLNKSAAWRFKFFLOSPVYVOYLODPKALFEE 478
QY 495 ATLAMDSHSSSIONSPKLTFRMKKDRASRGKKEKVRQLORTEHOAVLAEDKHLDDSD 554
DB 479 ATLSMOOTCEGIVG-----ALELERNGH-ASEGM 507
QY 555 ERP---SPEEERKHLIHLRLQRLHSIDLEIOEGKLVGICGVSQKTSLSIALG 610
DB 508 TRPDALGPEBEGRS-----LGPETHKINTLVVSGMMGLGVGNGSGKSSLSAILE 559
QY 611 QMTLBSGSIASGFPAVAAQAMLTNLTNDNIFGKEXDEERNVSNLSCLPDLATL 670
DB 560 EMHLEBSVGQSLAVPQQAWTVSGNIRENIMLGGAYDARKLQVHLCCSLRDLLEL 619
QY 671 PSSDLTEIGEGANLSSGQORISLARALYSDRSIYLLDPLSALDAHVGNHFNPSAIRK 730
DB 620 PFGMTETIGERGLNLSGQKORISLARAVSDRQIYLLDPLSALDAHVGNHFNPSAIRK 679
QY 731 HLKSTVLFVTHQLOYLVDDEVTFMRKSGTERTGHEELMNLNGDYATIPNNLLGEP 790
DB 680 TLRGKTVVLTHTQYLEFCQIILLENKICENGTHSELMQKKGKQAOLIOKKHKEATS 739
QY 791 PVETNSKRTSGSKODKPKRTSGIKKEKAVKPEEGQVQLEKGGQSVPMVGVYI 850
DB 740 DMLDQTAFLAKRPVESQALATSLSESLNGNA--PEHOLTOEEMEGSLMKRVYHHYI 797
QY 851 QAAQGPALFVIMLFLMNGSTAFSTWMLSYWIKOGSGNTTYRGNETSVS--DSMKDNP 909
DB 798 QAAQGVAVSCITFFVVLIVLFTFSFWMLSYWLEQSGTSSHESNGTMDAGNIDNP 857
QY 910 HMQYASIVASMAVMLLKAIRGVVYKGTLRASSRLHDELFRILRSPKPFEDTPTG 969
DB 858 QLSFYQVLYGNALLILCVGSSGIFFTKRYKASTLHNLFKFKVRCPSFEDTIPIG 917
QY 970 RLNRFEKMDQEVNVRPFOAEMFIQNVILFECVGMAGVPEVLAAGVPLVLFSLH 1029
DB 918 RLNCFAGDLEQDQPLIFSEQFLVSLMVAIVLVSLPILMLGALIMYICITY 977
QY 1030 IVSRVILRELKRLDNITQSPPLSHITSSIOGLATIHAYNKGQEFLLHRYOELDNQAPFE 1089
DB 978 MMEKKAIGVFERLENYRSRPLFSHILNLSIOGLSSIHYGKEDDISQFKRLTDQNNVYL 1037
QY 1090 LFTCAMRLAVRLDLISALTITTTGMLVLMHGQIPRAYAGLAISYAOULTGDFQFVRL 1149
DB 1038 LFLSTFTMAALRILNINVLVLAVALFAFGISSTPYRSFKYMAVNIYLOLSSFOATARI 1097
QY 1150 ASFEARTSVTERINHYIKTSLLEAPARIKKASPDPPOGEVTFEENAEKRYRENNPLV 1209
DB 1098 GLETEAQTAVERTILOYMKCVSEAPLHMEGSTCPQGPQOGEITIFQDYHMKYRDNPTV 1157
QY 1210 LKVSFTIKPREKIGIVGRTSGSKSSIGMALFRLVELSGGCIKIDGVRISDGLADLRK 1269
DB 1158 LHGINLITRGHEVGVIGYRTSGSKSSIGMALFRLVEPMAGITLIDGVDIGSIGEDLRK 1217
QY 1270 LSIIPQEPVLFSGTVRSNLDPPNOYTEDQIWDALERTHMKECIAOLPKLESEYMGDN 1329
DB 1218 LSVIPQEPVLFSGTVRSNLDPPNOYTEDQIWDALERTHMKECIAOLPKLESEYMGDN 1277
QY 1330 FSVGEROLLCIARALRCKLILIDEATAANDTETDILIOETIREAPDCMILTARHL 1389
DB 1278 FSVGEROLLCIARAVLRNRSKILIDEATASIDMETDOLIOETIREAPDCMILTARHL 1337
QY 1390 TVLGSDRIMVLAQGVVEFDTPSVLLSNDSSGRFAMFAAANKV 1433
DB 1338 TVLNCDHITLVGNKGVVEFDREYVLRKKPGSLFALMATATSSSL 1381

RESULT 7
US-10-162-012-34
Sequence 34, Application US/10162012
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.

APPLICANT: Silos-Santiago, Immaculada
 APPLICANT: Gu, Wei
 TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
 FILE REFERENCE: 10448-190001
 CURRENT APPLICATION NUMBER: US/10/162,012
 PRIOR FILING DATE: 2002-06-04
 PRIOR APPLICATION NUMBER: US 60/209,845
 PRIOR FILING DATE: 2000-06-06
 PRIOR APPLICATION NUMBER: US 09/875,321
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: PCT/US01/19340
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: US 60/209,257
 PRIOR FILING DATE: 2000-06-05
 PRIOR APPLICATION NUMBER: US 09/875,423
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: PCT/US01/19398
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/209,238
 PRIOR FILING DATE: 2000-06-05
 PRIOR APPLICATION NUMBER: US 09/875,363
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: PCT/US01/18247
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/227,068
 PRIOR FILING DATE: 2000-08-22
 PRIOR APPLICATION NUMBER: US 09/928,530
 PRIOR FILING DATE: 2001-08-13
 PRIOR APPLICATION NUMBER: PCT/US01/25475
 PRIOR FILING DATE: 2001-08-15
 PRIOR APPLICATION NUMBER: US 60/226,770
 PRIOR FILING DATE: 2000-08-21
 PRIOR APPLICATION NUMBER: US 09/934,421
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: PCT/US01/26096
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: US 60/279,281
 PRIOR FILING DATE: 2001-03-28
 PRIOR APPLICATION NUMBER: US 10/109,029
 PRIOR FILING DATE: 2002-03-28
 PRIOR APPLICATION NUMBER: PCT/US02/09728
 PRIOR FILING DATE: 2002-03-28
 PRIOR APPLICATION NUMBER: US 60/290,288
 PRIOR FILING DATE: 2001-05-11
 PRIOR APPLICATION NUMBER: US (not assigned)
 PRIOR FILING DATE: 2002-05-13
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 34
 LENGTH: 1360
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-162-012-34

Query Match 34.8% Score 2540.5; DB 6; Length 1360;
 Best Local Similarity 39.4% Pred. No. 2.8e-180;
 Match 542; Conservative 251; Mismatches 487; Indels 97; Gaps 11;

Db 239 SSFAFEKIQFKSVIHTSGBGDICAHLAVLAQISFTGDVNYLFEGVCGPLVLTTC 298
 Qy 302 VVALGMIVYVILGPGFGLSANGVILFYPMAMASRLTAIFRKCAVADDEROKANEV 361
 Db 299 ASLVICISISFYIIGYAFALICLVPLFLAVMTAMVAKOHHTSEVSQRIATVSEV 358
 Qy 362 LTVYKFKMYAMVAFSOSQOKIREERRILEKAGYFOSIYVGAPIVYVAVTSVH 421
 Db 359 LTCIKLIMTWKEPFKIIEGM-----ESLTFCKP----- 390
 Qy 422 MTLGFDLLAAQAFVTVTFVFNPMFALKVTPESVKSLEASVANDRFKSLFMEVHMK 481
 Db 391 -----GDMAFMSLMSLNLRLSVEFVPLAVAGLNSASAVRFFKFFLOESPVPYVQ 443
 Qy 482 KPASPHIKIEKNAATLAWDSHSSIQNSPKLTPMKKDKRASRCKKKEVROLATHEQAV 541
 Db 444 TLDPSSKALVEEATLSMOOTCPGIVNG-----AL 473
 Qy 542 LAEQGHLLDSDERP-----SPEEKGKHIHLGLRLQRTLSIDLEIOEGKLVIQGSV 597
 Db 474 ELERNGH-ASEGMRTPDADLGEPEGNS-----LGEPLHKLINLVSGMILGVCNT 524
 Qy 598 GSGKTSLSIALGQMTLLEGSIAISGTFAVYAAQAMILNLRDNLFGKEDEBERNSV 657
 Db 525 GSGKSSLSIALLEEMHLEGSVGVQSLAVYPOQAMIVSGNIRENIMLGAYDKARLYQ 584
 Qy 658 LNSCCLPDLAIIPLSPULTEIGEGANLGGQORISLARLYSDRSYIILDPALSADA 717
 Db 585 LHCCSLNRDELLEPFQGMTTEIGERGLNLSGQOKRISLARVYSDROYLLDPLSAVDA 644
 Qy 718 HVGNIHNSAIRKHLKSKTVLEFVTHOLOLYVDCDEVFMKGCCTTEGTGHELMNLNDY 777
 Db 645 HVGNIHEECIKTKLRKTYVLYTHOLOLYLEFCQIILLENKGLCENGTHSELMOKKGY 704
 Qy 778 ATFFNNLLGETPPEVLEINSKETSQSQKSDQPKGTGSIKKEAVNPEEGOLVLEEGK 837
 Db 705 AOLQKHKEATSDMLQDTAKIAEKPVESQALATSEESLNGNAV--PEHQLQEEEME 762
 Qy 838 QGSVPMSVYGYVIOAGGAPLAVLYMALPMNLNGSTAFSTYMWLSYVYKQSGNTTVRGN 897
 Db 763 EGSLSMRYVHYHIOAGGVYVSCIIFFVYLVLELTFFSEFWLSYVLEQSGTSSRESN 822
 Qy 898 ETSVS-OSMKDNPIMQYVYASIALSMAYMLIKAIRGVFEKGLRASSRHDELFRIL 956
 Db 823 GTMADLGNINADNPOLSTFYQVYGLNALLICVYSCSGIFPKVYRKASTALHMKLFNKVF 882
 Qy 957 RSPMKFPDTPPTGRILNRFKSDMDVDVRLPEQAMETIQVYVLFVFCVMAGVFPWFLV 1016
 Db 883 RCPKSPFDTPIGRLNCFAGDLEQLDQLPIFSEQFLVSLMVAIVALLIYVSLPYLL 942
 Qy 1017 AVGPLVILFSVLAIVSVKVLRELKRLDNITQSPFLSHITSIGCLATIIHAYNKQDFLHR 1076
 Db 943 MGALINVICIYYMMFKAIGVFRLENYSRSPLSHLSLQGLSIHVGKTEDPTSQ 1002
 Qy 1077 YOELLDNQAPFLFTCAMRLAVRLDISIALITTTGGMVLMLHGGQIPRAYAGLASYA 1136
 Db 1003 FKRLTDQNNYLLFLFSLSTRMMLRLIMTVLVALAVFABISSTPSFKMAVANYV 1062
 Qy 1137 VQLTGLFOFTVRLASETEARTSYERINHYIKTSLBAPARIKKAPSPDMPQGEVTFE 1196
 Db 1063 LQLASSFOATARIGLFEADQFAVERILQYMKMCVSAPLHMEGTSCPOGPOGHEILFQ 1122
 Qy 1197 NAKMRYRENLPVLYKAVSFITKPREKIGYGRGSGSSIGMALFRLVELSGCICIKIDGV 1256
 Db 1123 DYHKKYRDNPTVYLGINTLRGHEVVGIVGRGSSGSLGMAFLRIVERPAGHILIDGV 1182
 Qy 1257 RISDGLADRSKLSIIPQEVLESGTVRSVNLDPFNQYTEDQINDALEFTFMKCIAPLP 1316
 Db 1183 DICISIGEDLRKSLSVIPQDPVLLSGTIRKRLDPFDHHTDOQINDALEFTFLTAISKFP 1242
 Qy 1317 LKLESEVMEGDNESVGEROLLCTARALLRHCKTILIDEATVAADTETDILLIOETIREAF 1376
 Db 1243 KLHTDVENGENFSVGEROLLCTARAVLRNSKIILIDEATVASTIDMETDILLIOETIREAF 1302

Query Match 28.0% Score 2049.5; DB 5; Length 1325;
Best Local Similarity 35.4%; Pred. NO. 1.2e-143;
Matches 489; Conservative 254; Mismatches 466; Indels 171; Gaps 33;

US-09-6471140A-2

US-09-6471140A-2
; Sequence 2, Application US/096471140A
; GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruh, Gary D.
; APPLICANT: Lee, Kun
; APPLICANT: Belinsky, Martin G.
; APPLICANT: Bain, Lisa J.
; TITLE OF INVENTION: MR-Related ABC Transporter Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
; FILE REFERENCE: FCCC 98-02
; CURRENT APPLICATION NUMBER: US/09/647,140A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US99/06644
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,759
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/095,153
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1325
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-6471140A-2

Query Match 28.0% Score 2049.5; DB 5; Length 1325;
Best Local Similarity 35.4%; Pred. NO. 1.2e-143;
Matches 489; Conservative 254; Mismatches 466; Indels 171; Gaps 33;

US-09-6471140A-2

US-09-6471140A-2
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; GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruh, Gary D.
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; APPLICANT: Belinsky, Martin G.
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/095,153
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
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; LENGTH: 1325
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-6471140A-2

US-09-6471140A-2

US-09-6471140A-2
; Sequence 2, Application US/096471140A
; GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruh, Gary D.
; APPLICANT: Lee, Kun
; APPLICANT: Belinsky, Martin G.
; APPLICANT: Bain, Lisa J.
; TITLE OF INVENTION: MR-Related ABC Transporter Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
; FILE REFERENCE: FCCC 98-02
; CURRENT APPLICATION NUMBER: US/09/647,140A
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; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,759
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; PRIOR APPLICATION NUMBER: 60/095,153
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1325
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-6471140A-2

US-09-6471140A-2

US-09-6471140A-2
; Sequence 2, Application US/096471140A
; GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruh, Gary D.
; APPLICANT: Lee, Kun
; APPLICANT: Belinsky, Martin G.
; APPLICANT: Bain, Lisa J.
; TITLE OF INVENTION: MR-Related ABC Transporter Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
; FILE REFERENCE: FCCC 98-02
; CURRENT APPLICATION NUMBER: US/09/647,140A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US99/06644
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,759
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/095,153
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1325
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-6471140A-2

CURRENT APPLICATION NUMBER: US/60/389,987
 CURRENT FILING DATE: 2002-06-17
 NUMBER OF SEQ ID NOS: 3025
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 1718
 LENGTH: 1388
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-60-389-987-1718

Query Match 27.8%; Score 2034.5; DB 7; Length 1388;
 Best Local Similarity 34.3%; Pred. No. 1,6e-142;
 Matches 480; Conservative 259; Mismatches 471; Indels 189; Gaps 21;

85 LSALAPRTCTCKHNPVDNAGLFCSCMTFSWLSLAVAHKKGELSMEDVSLKHSDDV 144
 Db 92 MWALK-----ENPCSSASFLSRITFWMTGLI-VRGVROPFLGSDLSLNKEDTSQ 144
 QY 145 NCRRLERLMOELNEV-----GRDA-----S 166
 Db 145 VYPVLTKMKKKECAKTRKQPVKVVYSSKDPADPKSSKVDANEVVALVKSPOKEMNP 204
 QY 167 LRRVWIFCRTLITIVCLMITOLAGFSGPAMVAKHLEYTQATSNLOYSLLVIGLL 226
 Db 205 LKRVLYKTEGPFYLFMSFEKAIHDLMMFSGPQ-ILKLILKFVNDTKAPDMQGYFTVLLF 263
 QY 227 LREIYRSMGLALMALNTGYRLKGAILLMAFKLILKLNKEK--IGELINICSDG 284
 Db 264 VYACIOTLVHOFYHICFSGMKIKYAVIGAYRKALVITNSARKSVEIYNLSVDA 323
 QY 285 OMFEAAVGSLLAGPVAAILGIMVNIILGPTGLSASVLETFPAMFASRLAYR 344
 Db 324 QRFMDATITINMWSAPLOYILALYLLMLNLGFSVLAGAVALMAYVNAVMAKKTQ 383
 QY 345 RRCVATDERVOKMNEVLYIKFKYAWKAFSGQVOKIREERILKAGYFQSIYVG 404
 Db 384 VAHMKSNDRIKLMNEILNGIKVLYAMELAFKDKVLAIRQBELVLKSAVLSAVGF 443
 QY 405 VAPIYVIVASVTFVSHMLGFD--LTAQATVIVTFVNSMFPALVYTPSVKLSASY 462
 Db 444 TWVCPPELVALCTFAVYVVIDENNILDAQTAFSLAFILRLPRLILMPVIVSSIOASV 503
 QY 463 AVDRFSLMEEVH--MKNNPASP--HIKEMNATLAWSSSSSIONSKPLPKK 517
 Db 504 SLKRLRIFLSHELEPDSTERRPVKDGCTNSTYVNAFTW----- 545
 QY 518 KDRASRGAKEKERVOLORTHOAVLAEOKGHLLDSDERPSPREEBKHIHLGRLORT 577
 Db 546 -----ARSDP----- 552
 QY 578 LHSIDLEIOEKLIVGICGVSGKTSLSIALIGOMTLLEGSLAISGTFAVVAQOAILNA 637
 Db 553 LNGITFISPEGALIVAVVGCGKSSLLSALLAEMDKVEGHVAIKGSVAVVPOAWIOND 612
 QY 638 TLRDNTLPEKEDERYNSVNSCCRLPALILPSSDLTEIGRGANLSGGQORSLAR 697
 Db 613 SLRENILFCCQLEERYNSVIOCALPLDEILPSSGDRTEIGKGNVLSGGQORSLAR 672
 QY 698 ALYSDRSIYLLDPLSALDAVNHILFNSAI--RKHLKSKTVLFVTHOLOYLVDCEVIF 755
 Db 673 AVYSNADYILFDPLSAVDAHGHKHFENVIGPKGMLKNKTRILVHSMYLPQVNVITV 732
 QY 756 MKEGCTTEGTHBELMLNNGDYATIF-----NNL 784
 Db 733 MGGGKISGMSYOELIARGAFAELRYASTEOBODAEENGCTVGVSGPEAKOMENCM 792
 QY 785 LL-----GEPVPEINSKKRTSGSKSOKKPKRTSGIKKEKAVKPEEGOLVQLEEGGGS 840
 Db 793 LVTDSAGKOLQOLSSSSSYSGDISRHN--STAELOKAEAKKETWMLKENDAKQOTQ 849
 QY 841 VPMVSYGVYIOAGGFLAFLVIMALEFMLNVGSTAFSTWMLSYVIKGSGNTYTVTNGNETS 900

Db 850 VKLSYVDYWKAKIGLFTLSLIF-LFMCHNVASLANSYMLSTMTDPIVNGT---QERTK 905
 QY 901 VSDSMKDNPHMOYYSIYALSMAVMLLKAIRGVVEYKGTLRASSRLHDELFRILRSPM 960
 Db 906 VRLSVYCALGISOGIAVFGVSMVSI-----GGILASRCLHVDLHSLIRSPM 953
 QY 961 KPFDTPTGRLNRFSGKDNQEDVNRLLPQAEMLQWLVLFPCVGMAGVPPFVAVGP 1020
 Db 954 SFEERTPSGNLVNRFSEKLDVTDSMIPEVIMKMGSLFNVIACIYILLATPIAAITIP 1013
 QY 1021 LVILFSLVHLIVSRVLI---RELKRLDNTQSPPLSHITSSIOGLATTHAANKQOEFLHRY 1077
 Db 1014 LGILY---FFVQGFVYASSNQLKRLSVSRSPYSHNENLLGVSVIRAEDEERFIHOS 1070
 QY 1078 QELLDNQAFLEFTCAMRLAVRLDLISLITTTGLMIVLMHGOIPRAYAGLAISYAV 1137
 Db 1071 DLKVDENOKKAYPSIYVANRLAVRLCVCNCIYFALFVAVIRSHSISAGLVLSYSYL 1130
 QY 1138 QLTGLQFTYRLASETEARTSVLRINHYIKTSLSEAPARKKAPSPDPOGEVTFEN 1197
 Db 1131 QVTTYINMLVLRMSSEMETNIVAEVRLKEYSET-EKEAPMOIOETAPSSMPQVGRVEFRN 1189
 QY 1198 AEMRYRENPLVLYKKYSFTIKPEKIGIVGRTSGKSSGLMALFRLVELSGCIRKIDVR 1257
 Db 1190 YCLRYEDELDFVLRHINVTINGEKVGIYRTGAKSSLLGLFRINESAGEIILIDGIN 1249
 QY 1258 ISDIGLADRSKSTIIPQEVLFSGTVRSMLDPPNOTEDQIDALERTHMKECIAQLPL 1317
 Db 1250 IAKIGLHDLRFKTTIIPQVLFSGSLRMLNLDPSQYSDSEVWTSLELAHLKDFVSALPD 1309
 QY 1318 KLESEVMENGDNSVGEEROLCTARALLRHCKLITLIDEAAMDTEDDLIOETIRAF 1377
 Db 1310 KIDHECAEGEENLSVGOROLVCLARLLRKTILVDEATAVADLETDLOSTIRTOPE 1369
 QY 1378 DCTMLTIAHRLHTVLGSDR 1396
 Db 1370 DCTVLTIAHRLNTIMDYTR 1388

RESULT 10

US-09-935-625-26957
 Sequence 26957, Application US/09935625
 GENERAL INFORMATION:
 APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
 FILE REFERENCE: 2750-1481P
 CURRENT APPLICATION NUMBER: US/09/935,625
 CURRENT FILING DATE: 2001-08-24
 NUMBER OF SEQ ID NOS: 33136
 SEQ ID NO 26957
 LENGTH: 1510
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: peptide
 LOCATION: 1..1510
 OTHER INFORMATION: Ceres Seq. ID no. 3447801
 US-09-935-625-26957

Query Match 27.7%; Score 2023.5; DB 5; Length 1510;
 Best Local Similarity 34.4%; Pred. No. 1.2e-141;
 Matches 478; Conservative 239; Mismatches 500; Indels 171; Gaps 21;

74 EEPKRGKYNHGLSALPRTCTCKHNPVDNAGLFCSCMTFSWLSLAVAHKKGELSMEDV 133
 Db 105 EELRPG-----NICEPRH-----ANLFDSTFSWMLPMTLIGSKR-PLREKOV 147
 QY 134 WSLKHSDDVNCRLRLMOEELNEVGRDAASLRVWVIFCTRLLISVCLMITQLAG 193
 Db 148 WHLDYDTKTEITLRSRQSKWMDKLEKPKP-----W-----LLRALNNSLGG 188

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QY 194 -----FSGPAFWKHLEETQATES---NLQYSLILVGLLLEIVRSW 234
Db 189 RFWVGFWKIGNDSCQVGP-LLINELLSKMQNEPAMIGYIYALSFVGVGLCE-- 245
QY 235 SLALTALNRTGVRGLGAILTMAFKILIKINIKESL--GELINICSDGOMFEPA 292
Db 246 --AQYONVAVRQYRLRSALIAVFRKSLRLTEGRRKFPQTKITNMTDAESLQICQ 303
QY 293 VGSLLAGPVVALIGMIVNYIILGPTGFGSAVFILFYPMAMFASRLTAVFRRCVATD 352
Db 304 SLHTMSAPRRIIVALLVLYIQQLGVASIIGALFLVLMFPLOIOTVYISKTQKLFEGGLRTD 363
QY 353 ERVQKNEVLTITKIKMAYAKAFSOSVOKIREERRIIEKAGYFOSITVGAPIVVI 412
Db 364 KRIGLMEVLAAMDVQCYAMENSFOSKYQTVRDEDELSPRKAQLLSAFMFMILNSIPVL 423
QY 413 ASVTFESVHMTLGFDLTAQAFTVYVNSMTFALKVTPSPVSLSEASVAVDRFKSLFL 472
Db 424 VTVVSFVFSLLGDLTPAPAFITSLFSVLRPLFLMPLPITITOMANVANSINLEEVLS 483
QY 473 MEVHMINKNPASP-HIKIEMKNTLAMDSSHSSSIONSPKLTFRMKDKRASRGKKEVR 531
Db 484 TEERVLLPNPIEPGPALISIRNGYFSWDS----- 513
QY 532 QLORTEHQAVLAQKGLHLLDSDEPSPREEBKHHHLRLQRTLHSDLEIQEGKLV 591
Db 514 -----KADRP-----TLNINILDIPLGSLV 533
QY 592 GIGSGVSGKTSLSAIIIGOM-TLLEGSIAISGTFAYVAQAOMLNTLNDILFGKED 650
Db 534 AVVSGTGEKTSLSAIIIGOM-TLLEGSIAISGTFAYVAQAOMLNTLNDILFGKED 593
QY 651 EERYNSVLSNCCRLPDLALIPSSDLTEIGRGANLSSGQORISLALALYSDRSITLDD 710
Db 594 QEKYERTYDVTALQHEDELLPGDLPTEIGRGVINSISGQORVMSAAVYVNSNVCILDD 653
QY 711 PLBALDAHNGNIHFNPAIRKHLKSKTYLVYTHOLOLYLVDCDEYIEMEGCITTEGHEEL 770
Db 654 PLBALDAHNGOQVFEKCIKRELQOTTRVLVTLNQLHFLSQYDKILVBEQVKEGTYEEL 713
QY 771 MNNGDVAITFNNL-----LLGEPVPEINSKRETSQSKQSKGKGTGIRKEKA 822
Db 714 CHSGPLFORLMEBNAKVEDYSENGEAEDVQTSYKPEVENCNANNLQDGEITKNSKGN 773
QY 823 VKPEEGOLVQLEEKGGQSVPMYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 882
Db 774 V-----LVKREERETGVSMKVLERYQNALGGAMVMMVLYCVLQVRRVSSSTLSE 827
QY 883 WIKOGSGNTVTYQNETSVSDSKMKNPHMOYVASTALSAVMLILKAIRGVVFKGTLR 942
Db 828 WTDG---TFKTHG-----PLFYNIIVALLSFGQVSVYLLINSYMLIMSLEY 870
QY 943 ASSRLDELFRILRSPKPEFDPPTPTGRILNRFPSKMDDEVDRPLPQAEPIQVILLVF 1002
Db 871 AAKKHMDAMGLSLRAKWEFFQTNPLGRILNRFKAKMDGIDRIVAVFVNMWGSTIAOLLS 930
QY 1003 CVMGIVGFWPFLVAVGPTLFSVLHVSRLIRELKRDLNITQSPFLSHITSIOGLA 1062
Db 931 TVLIGIVSTLSLMAIMPLLVFGAYLYQNTSREIKRMDSTRSPVYVQFGLAGLS 990
QY 1063 TTHAYNKQGLFRLRYOELDDNOAPFLFLCQKMBLAVRLDLISIALITTTGLMTVMHG 1122
Db 991 SIRAYKAYDRMAELINGRSMONNIRFTLVNNAANRMGLIRLEVGLGLVWMLTASLAVQNG 1050
QY 1123 QI---PRAYA---GLAISYAOLGLPOFTVRLASEPFAETSVBRINHYIKTISLEPAR 1177
Db 1051 KAAHQVASTMGLSLTALSTSLTAVRLASLANSINSEKVENYVYIETP-EAPLV 1109
QY 1178 IKRKASPDMPQEGEVTFENAEKRYRENPLVLVKVYFTIKPEKIKIVRTGSGKSLG 1237
Db 1110 IENRRPFGPGRSSGSIKEFEVYLRYRELPPLVHLGVSFLISPMKQVIVGTGSGKSSL 1169
QY 1238 MALFRLVELSGGCIKIDVIRISDGLADLRKSLIIPQEPVLSGTVRNSLDPENQYED 1297

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Db 1170 NALFRIVELEKGRLLIDECTIGRGLMDLKRKVLGITQAVYVLSGTVRFNLDPPSEINDA 1229
QY 1298 QIMDALERTHMKECIAOLPLKLESEVMEGNDNSVSGRCLLJARALLRCKIILDEAT 1357
Db 1230 DLMSELERAHKDTIRRNPLGLDAEVEAGENFSGVGRQLLSLARALLRSKILVLEAT 1289
QY 1358 AAMDTEFDLLOETIRAFADCTMTLTAHRLHYVLSDRIMVLAQGVVEEDPVSLLN 1417
Db 1290 AAVDRVTDVLOKTIREEFSCMLLIIAHLNLTIIDCKVLYDSGKVOEFSPEENLLN 1349
QY 1418 DSSRFYAM 1425
Db 1350 GESSFSKM 1357

RESULT 11
US-09-935-625-26956
; Sequence 26956, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
; TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 26956
; LENGTH: 1529
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..1529
; OTHER INFORMATION: Ceres Seq. ID no. 3447800
US-09-935-625-26956

Query Match 27.7%; Score 2023.5; DB 5; Length 1529;
Best Local Similarity 34.4%; Pred. No. 1.2e-141;
Matches 478; Conservativity 239; Mismatches 500; Indels 171; Gaps 21;

QY 74 EENPKRYHHGLSALKRITRTCKHQHPVDNAGLFSCFTFSWLSLAVARHKGELSMEDV 133
Db 124 EELPGE-----NICPERH-----ANLFDISFFSWLPLMLTIGSR-PLTEKDV 166
QY 134 WSLSKHSSDVNCRRLERIMOELNEVGPDAASLRVAVMIFCRRILLSIYCLMITQLAG 193
Db 167 WHLDTWKTEFLMHSFQKSMDELEKRP-----W-----LIRALNLSLG 207
QY 194 -----FSGPAFWKHLEETQATES---NLQYSLILVGLLLEIVRSW 234
Db 208 RFWVGFWKIGNDSCQVGP-LLINELLSKMQNEPAMIGYIYALSFVGVGLCE-- 264
QY 235 SLALTALNRTGVRGLGAILTMAFKILIKINIKESL--GELINICSDGOMFEPA 292
Db 265 --AQYONVAVRQYRLRSALIAVFRKSLRLTEGRRKFPQTKITNMTDAESLQICQ 322
QY 293 VGSLLAGPVVALIGMIVNYIILGPTGFGSAVFILFYPMAMFASRLTAVFRRCVATD 352
Db 323 SLHTMSAPRRIIVALLVLYIQQLGVASIIGALFLVLMFPLOIOTVYISKTQKLFEGGLRTD 382
QY 353 ERVQKNEVLTITKIKMAYAKAFSOSVOKIREERRIIEKAGYFOSITVGAPIVVI 412
Db 383 KRIGLMEVLAAMDVQCYAMENSFOSKYQTVRDEDELSPRKAQLLSAFMFMILNSIPVL 442
QY 413 ASVTFESVHMTLGFDLTAQAFTVYVNSMTFALKVTPSPVSLSEASVAVDRFKSLFL 472
Db 443 VTVVSFVFSLLGDLTPAPAFITSLFSVLRPLFLMPLPITITOMANVANSINLEEVLS 502
QY 473 MEVHMINKNPASP-HIKIEMKNTLAMDSSHSSSIONSPKLTFRMKDKRASRGKKEVR 531
Db 503 TEERVLLPNPIEPGPALISIRNGYFSWDS----- 532

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QY 532. QLOPTEHQAFLAEOKGHLLDSDERPSPEEKGKHIHLGHLRLQRTLSIDLEIOGKLV 591
Db 533. -----KADRP-----TLNINIDIPGSLV 552
QY 592. GICGVSQKTSLSIALIGOM-TLEGSTAISTEAYVAQAQAMILNATLRDNLIFGKEYD 650
Db 553. AAVGSGEKTSLISAMIGELPARSDATVTLRGSVAAYVQVSWIFATVRDNLIFGAPD 612
QY 651. EERYNSVNSCCRPDLALPSSDLTEIGERGANLSGGORORISLARALYSRSTIYILD 710
Db 613. QEKYERVIDYVALQHDLELPGDLEIGERGVNISGGOKORVSMARAYSNSDVCILDD 672
QY 711. PLSALDAHGNHIFNSAIRKHLKSKTVLFTVHQLOYLVDCDEVIFMKKEGCIERTGHEEL 770
Db 673. PLSALDAHVGQGVFEKCIKRELGGOTTRVLTQNLHFLSOVDKTLVHEGTVKEGTYEEL 732
QY 771. MNLNGDYATIFNNL-----LIGETPVEINSKKEKTSQKSDKPKTSIKKEKA 822
Db 733. CHSGPLFORLMEAGKVEDYSENGEAAYDQTSVKPVENNANNLOKDIETKNSKEGNS 792
QY 823. VKPEEGOLVQLEKKGSGPWSYGVYIOAAGPLAFLVYMLFMNLNGSTAFSTWMLSY 882
Db 793. Y-----LVKREERTGVVSMKVLERYONALGAWVMVLVCYVLTQVFRVSSSTWMLSE 846
QY 883. WIKOSGNTVTYRGNETSVSDSMKDNPHMOYASIVALSMAVMLILKATRGVVEKGLR 942
Db 847. WIDSG-----TPKTHG-----PLFYNIYALISFGQVSVTLINSTWMLSSLY 889
QY 943. ASSRLHDELFRILRSPMKFEDPTPTGRILNRPSCDMDEVDRVLPQAEFMIONVILVEF 1002
Db 890. AAKKHDMALGSLIRAPVVEFQTNPLGRILNRPFAKMDGIDRTVAVFVMMFGSIAQLLS 949
QY 1003. CYGMAGVFPWVLAVGPIVILFVSLHYSKVLIREKLKLDNITQSPFISHTSSIOGTA 1062
Db 950. TVILIGIVSTLSLMAIMPLLVFVGYALYIYQNTSRBIKMDSTTSPVVAQGEALNGLS 1009
QY 1063. THAYANKQOEFLHRYQOELLDNQAPFLEFPCAMRLAVBLDLSIALITTTGIMTYLMHG 1122
Db 1010. STRAYKADRAEINGRSMNIRFTLVMAANRMLGTRLEVLGGMLVLTASLAVMONG 1069
QY 1123. QI--PRAVA--GLAISYAVOLTGLFOFTVRLASETEAFSTVERINHYIKRLSEAPAR 1177
Db 1070. KANQQAAYASTWGLLSYALSTSSLTAVLRSLAENSLNVERGNITELPS--EAPLV 1128
QY 1178. IKNRPPSDMPOEGEVTEENAMERENPLVLYKVSFTIKKEKIGYGRGSGKSSIG 1237
Db 1129. IENNRPPGWPSSGSIKFEDEVVLRARPELPVYLVHGVSEFLISPMKGVIGRFGAGKSSLL 1188
QY 1238. MALPFLVELSGGCIKIDGVRISDGLADRSKLSIIPQPVYFSGVVRNSNDPNOYTED 1297
Db 1189. NALFIVLEKGRILIDEDIGRFGIMDKRYLGITIPQAPVLFSGVVRNIDPFSEHND 1248
QY 1298. QIWDALERTHMEKCIAPQLPKLESEVMEGDNFVSGEROLLCIARALLRCKILLIDEAT 1357
Db 1249. DMESLEBAHLKDTIRNRPDLGDAVTEGENFSGORQLLSARALLRCKILLIDEAT 1308
QY 1358. AAMDTETDLLOETIREAPADCTMLTIAHRLHTVLSGDRIMVLAGOQVVEFTPSVLLSN 1417
Db 1309. AAVDRTVTLQKTIREFKSCMTLIIAHLNTIIDCKVLVLDGKQVGFSSPERLSEN 1368
QY 1418. DSSRYAM 1425
Db 1369. GESSFSKM 1376

FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935, 625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 26955
LENGTH: 1622
TYPE: PRP
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..1622
OTHER INFORMATION: Ceres Seq. ID no. 3447799
US-09-935-625-26955

Query Match 27.7%; Score 2023.5; DB 5; Length 1622;
Best Local Similarity 34.4%; Pred. No. 1,4e-141;
Matches 478; Conservative 239; Mismatches 500; Indels 171; Gaps 21;

QY 74. EEPKCKYHNGLSALKPIRTCKKHOPVDNAGLFSCMFPSSLSLARVAHKKGELSMEDY 133
Db 217. EELPGE-----NICPERH-----ANLFSIFSWLPLTLGSKR-PLTEKDV 259
QY 134. WSLSKHSSDVNCRRLERLMOEELNEVGPDASLRVWVIFCRTLILSIVCIMITOLAG 193
Db 260. WHLDTMDKTETLMRSFQKSMDELEKRP-----W-----LRLANSLG 300
QY 194. -----FSPAPFVKKHLEYQATES--NLOYSLLVGLLLEYVRSM 234
Db 301. RFWMGFWKIGNDCSQFVP-LLNELLKSMQLEPNAMIGIYAIISIFGVVGVGICE-- 357
QY 235. SLATMALVRRGVRLRGILTMAPKILIKKIKKSL--GELINICSDGORMEAA 292
Db 358. --QYFQNVNRGVRLRSALIAVFRKSLRLNEGKKKQGTGTYMLMTDASLQIQ 415
QY 293. VCSLLAGPVAAILGMIVVILGPTFGLSAVFILFYPMMPASRLTAVFRKCYAARD 352
Db 416. SLHTMSAFRIIVLVLYLQOLGVAISIIIGALEFLVMPFIQYIISKTKLKEGLOIRD 475
QY 476. KRIGLMEVLAAMDYKCYKAWENSFQKQVTVRDELSMFRKQILSAFNMFLNISIPV 535
Db 413. ASVYFESVMTGFDLTAQAFVTVYFNSMFPALKVTPFVSXSLSAAYANDREFSL 472
QY 536. VTVVSFGVSLGGDLTPARAFTSLSFSLVRPLEMLNIIITQVNNANVSLRLEVIS 595
Db 473. MEEVHIKKRPASP-HIKIEMKATLAMPSSHSISSIONSKPLPMMKKOKRASGKKEVR 531
QY 596. TEEVLLPRLPIEPQPAISIRNGYRWS----- 625
Db 532. QLOPTEHQAFLAEOKGHLLDSDERPSPEEKGKHIHLGHLRLQRTLSIDLEIOGKLV 591
QY 626. -----KADRP-----TLNINIDIPGSLV 645
QY 592. GICGVSQKTSLSIALIGOM-TLEGSTAISTEAYVAQAQAMILNATLRDNLIFGKEYD 650
Db 646. AAVGSGEKTSLISAMIGELPARSDATVTLRGSVAAYVQVSWIFATVRDNLIFGAPD 705
QY 651. EERYNSVNSCCRPDLALPSSDLTEIGERGANLSGGORORISLARALYSRSTIYILD 710
Db 706. QEKYERVIDYVALQHDLELPGDLEIGERGVNISGGOKORVSMARAYSNSDVCILDD 765
QY 711. PLSALDAHGNHIFNSAIRKHLKSKTVLFTVHQLOYLVDCDEVIFMKKEGCIERTGHEEL 770
Db 766. PLSALDAHVGQGVFEKCIKRELGGOTTRVLTQNLHFLSOVDKTLVHEGTVKEGTYEEL 825
QY 771. MNLNGDYATIFNNL-----LIGETPVEINSKKEKTSQKSDKPKTSIKKEKA 822
Db 826. CHSGPLFORLMEAGKVEDYSENGEAAYDQTSVKPVENNANNLOKDIETKNSKEGNS 885
QY 823. VKPEEGOLVQLEKKGSGPWSYGVYIOAAGPLAFLVYMLFMNLNGSTAFSTWMLSY 882


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Db 886 V-----LKRERETGVSMKLEKQNALGAMVVMVLYTVLQVFRVSSSTWLS 939
Qy 883 WIKOGSGNTVTGRNETSVSDSMKNPHMOYASIVALSMAVMILKAIGVVFVKGLR 942
Db 940 WTDGSG---TPKTHG-----PLFYNIYVALLSFGQVSVTLINSYMLINSLSL 982
Qy 943 ASSRLHDELFRILRSMPKFFDTPTGRILNRSKDMDEVVRLPQAEFIONVILVFF 1002
Db 983 AAKKMDAMGLSILRAPMVEFOTNPLGRILNRPKMDGIDRIVAAVNNFMGSIQGLS 1042
Qy 1003 CVMGAGVFPWFLVANGPLVLSVLIYSRVILRELKRDNTTOSFELSHITSIOGLA 1062
Db 1043 TVLILIGVSTLSMALMPLLVFYGAVLYQNTSREIKRDSYTRSPVYAQFGBALNGLS 1102
Qy 1063 TIHAVNGQGEFLHRYOELLDDNOAPFLFTGCAMRLAVRLDLISALITTTGLMIVLMG 1122
Db 1103 SIRAYKAYDMAELNGRSMNNIRFLVNNAAWRWLGIRLEVGLMWTATSLAWQNG 1162
Qy 1123 QI--PRAYA---GLAISYAVOLTGLFOFYVRLASETEAPTSVERLNHYIKTISLEAPAR 1177
Db 1163 KANNOQAVASTMGLLSLALSTISSLTAVLRSLAENSLSNVERGNYEIRFS-EAPLV 1221
Qy 1178 IKRKASPPMPQGEVTEFNAEMRYRENPLVLKVSFTIKPEKIGIVRTSGSKSLG 1237
Db 1222 IERNRPPPGHPSGSIKFEDEVYLRPELDPVLHGVSELSIPMDKVGIVGTGAGSSLL 1281
Qy 1238 MALFRLVELSGGCIKIDGVRIIDIGLADLRSLKSLIIPQEVLFSGTVRSMIDPFNOYTED 1297
Db 1282 NALFRIVELEKGRILIDECDIGRGLMDLRKVLGIIPQAVLFSGTVRFLDPESEHND 1341
Qy 1298 QITDALEPRHMKCIQOLPLKLESEVWENGDNVSVEGROLCTARALLRCKILLIDEAT 1357
Db 1342 DIMESLERHAKLKTIRNPLGDAEYTEAGENFSVGOROLSLARALLRCKILLIDEAT 1401
Qy 1358 AAMDFTDLIOETIREAFDCTMTLTAHRLKTVLGSRIWLAQGVFEPTSVYLLSN 1417
Db 1402 AANDVATDVLIQKTIREFRKSTMLIAHRLNTIIDCKVLVDSGKQVEFSSPENILSN 1461
Qy 1418 DSSRYTAM 1425
Db 1462 GESSFSKM 1469

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RESULT 13
US-09-935 625-26574
; Sequence 26574, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 26574
; LENGTH: 1510
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..1510
; OTHER INFORMATION: Ceres Seq. ID no. 3087738
US-09-935 625-26574

```

Query Match 27.6%; Score 2013.5; DB 5; Length 1510;
 Best Local Similarity 34.3%; Pred. No. 6,8e-141;
 Matches 476; Conservative 240; Mismatches 501; Indels 171; Gaps 21;

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Qy 74 EHPKQYHNGHLSALPRTCTCKQHPVDNAGLFCMTFSWLSLARVAHKKGELSMEDV 133
Db 105 EELPGE-----NIGPERH---ANLFDSIFFSWLNPLMTLGSKR-PLIEKDV 147

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Qy 134 WLSKHESSVNCRRLERLMOEELNEVGPDAASLRVWVIFCRTRLILSTVCLMITOLAG 193
Db 148 WHLDWKTETLMRSFQKSDKELEKPP-----W-----LLRALNNSLIG 188
Qy 194 -----FSGAPVWKHLETOATES---NLOYSLILGLILGLEIRSN 234
Db 189 RFWMGFWKIGNDOSQVGP-LILNELKSMOLNEPAMICYITAIISFVGVGLVCE-- 245
Qy 235 SLATWALNRYGTVRGLGALITLMAFKKILKLNKEKSL--GELINICSDGORMEAAA 292
Db 246 --AQYFQNVNRVGRRLRSALIAVFRKSLRTNDRGKRFQGTITNMTDASLQIQ 303
Qy 293 VGSILAGPVALICMTYNNIIGPTGFLGSANFLEFYPMMAASRLTAFRRCAVATD 352
Db 304 SLHTMSPAPRIIVAILVLYOQLGVASIIQALEVLMFPIDYIISKTQRLTEGRLTD 363
Qy 353 ERYOKMNEVLTITKIKMVAWKAFGSGYOKIREEERILEKKGYFOSITVGAPIYVVI 412
Db 364 KRGLMNEVLAAMDYKCYAMENSFQSKVOTVRDDELWFRKQOLLSAFNMFTLNSIPVL 423
Qy 413 ASVYTESVHMTLGFDDLTAQAFTVTVFNSMTFALKVTPFSVKSLSSEASYADVDFKSLFL 472
Db 424 VTVVSFGVSLGDDLIPARAFTSLSEFVLRPLPLPNIITQMVANVSLNRLEEVLS 483
Qy 473 MEYVHMINKRPAAP-HIKIMKANATLAWDSHSSIONSPLKTRPKKKDKRASGKKEKVR 531
Db 484 TEERVLLPNPPIEPGQPAISIRNGYFSWDS----- 513
Qy 532 QLORTEHQAVALAQKGLLLDSDRPSPEEKGKHHGLRLQRTLSHIDLETOEGKLV 591
Db 514 -----KADRP-----PLSNINILIPLAGSLV 533
Qy 592 GIGGSVSGKTSLSIALIGOM-TLEGSIAISGTFAYVAQOAMTLNATLDNTLFGKEYD 650
Db 534 AVVSGTEGKTSLSIALMGLPLPARSDATVTLRGSVAVPQVSMFPAVDNLTILFGAPFD 593
Qy 651 EERYNSVLSNCCRPDLALIPSSDLTEIGRGANLSGGQQRISLARALSDSSTYILD 710
Db 594 QERYERIVDYTALOHDELLPGGDLTEIGRGVNIISGGQKQRVSMARVANSNDVCLTE 653
Qy 711 PLALDAHVGNHIFNSAIRKLSKTVLFYTHOLOLYLVDCDEVYFMKGGCTIRGTFHEEL 770
Db 654 PLSLDAHVGOQYFEKCIKRELQOTTRVLYTNOLHPLSQYDKLILVNEGIVKREGYIEL 713
Qy 771 MNLNGDVATIFNNL-----LLGETPVEINSKKEKTSQSKSODKGPRTGSIKKEKA 822
Db 714 CHSGPLPRILMENAKGVEDYSEENGAEVHQTGVKPVENGNANMLQDGIETKNSKGN 773
Qy 823 VKREEGQVLEKGGQSVWMSYGVYIOAAGPPLAVLYMALPMLNVGSTASTWMLST 882
Db 774 V-----LVKRERETGVSMKLEKQNALGAMVVMVLYTVLQVFRVSSSTWLS 827
Qy 883 WIKOGSGNTVTGRNETSVSDSMKNPHMOYASIVALSMAVMILKAIGVVFVKGLR 942
Db 828 WTDGSG---TPKTHG-----PLFYNIYVALLSFGQVSVTLINSYMLINSLSL 870
Qy 943 ASSRLHDELFRILRSMPKFFDTPTGRILNRSKDMDEVVRLPQAEFIONVILVFF 1002
Db 871 AAKKMDAMGLSILRAPMVEFOTNPLGRILNRPKMDGIDRIVAAVNNFMGSIQGLS 930
Qy 1003 CVMGAGVFPWFLVANGPLVLSVLIYSRVILRELKRDNTTOSFELSHITSIOGLA 1062
Db 931 TVLILIGVSTLSMALMPLLVFYGAVLYQNTSREIKRDSYTRSPVYAQFGBALNGLS 990
Qy 1063 TIHAVNGQGEFLHRYOELLDDNOAPFLFTGCAMRLAVRLDLISALITTTGLMIVLMG 1122
Db 991 SIRAYKAYDMAELNGRSMNNIRFLVNNAAWRWLGIRLEVGLMWTATSLAWQNG 1050
Qy 1123 QI--PRAYA---GLAISYAVOLTGLFOFYVRLASETEAPTSVERLNHYIKTISLEAPAR 1177
Db 1051 KANNOQAVASTMGLLSLALSTISSLTAVLRSLAENSLSNVERGNYEIRFS-EAPLV 1109
Qy 1178 IKRKASPPMPQGEVTEFNAEMRYRENPLVLKVSFTIKPEKIGIVRTSGSKSLG 1237

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Db 1110 IENNRRPPGMPSSGSIKIFEDVVLARKRPDLRPLVHLGVSFLLSPMDKGIYGRGAGKSSLL 1169
Qy 1238 MALFLVELSGGCIKIDGRISDGLADLRKSLIIPQPVLFSGVRSNDLPNOTED 1297
Db 1170 NALFLVELTEKRLILDECDIGRFGLMDLRKYVGLIPQAVLFSGVIRNLPDFSEHND 1229
Qy 1298 QIWDALERTHMEKCIADLPKLESEVMENGDNFVSGEROLLICARALLRCKILLIDEAT 1357
Db 1230 DLMESLEHRLKDTIRRNPLGDAEYTEGENFVSQOROLLISARALLRCKILLIDEAT 1289
Qy 1358 AAMDTELDLLIQTIREAFADCTMLTIAHRLHVLGSDRIMVLAQGVVEFDPSPVLSLN 1417
Db 1290 AAVDRTDVLIOKTIREEFKSCMTLIIAHLRLNTIIDCKVVLVDGKVOEFSSPENLSN 1349
Qy 1418 DSSRFYAM 1425
Db 1350 GESSFSKM 1357

RESULT 14
US-09-935-625-26573
; Sequence 26573, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 26573
; LENGTH: 1529
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..1529
; OTHER INFORMATION: Ceres Seq. ID no. 3087737
US-09-935-625-26573

Query Match 27.6%; Score 2013.5; DB 5; Length 1529;
Best Local Similarity 34.3%; Pred. No. 7e-141;
Matches 476; Conservative 240; Mismatches 501; Indels 171; Gaps 21:

Qy 74 EHPKGYHHGLSALKPIRTCKHOPVDNAGLFCSTPFWLSLARVAHKKGELSMEDY 133
Db 124 BELPGE-----NICPERH---ANLFDSIFPSWLNPLMTLSKR-PLREKDY 166
Qy 134 WSLSHSSDVNCRRLERIMOELNEVGDAASLRVWVIFCRTLILSYCLMTQLAG 193
Db 167 WILDWMDKTETLMRSFQKWDKELEKPKP-----W-----LLRLANSLSG 207
Qy 194-----FSGPAMVKKHLEFYQATES---NLOYSLLVGLLTELVRSM 234
Db 208 RFWMGFGWKIDGCSQFVGP-LILNELLSMOLNEPAMIGYIAISIFVGVGVCE-- 264
Qy 235 SLATWALNVRTGVRLGAILTMAFKKILTKNIKESL--GELINIGSNDGQRMFEAA 292
Db 265--AQFQONNMRVGRFRLSLIAAVFRKSLRLTNEGKRRQTKITMLMTTDAESLQIQ 322
Qy 293 VGSLLAGEVVAAILGMITVITLPGPLGSAVFLIFPAMMFASRLTAYFRKKVAAAD 352
Db 323 SLHTWMSAFRITVALVLLYQOLGVAISIGALFLVLMFPIQIVTILSKTKLFEKGIQFD 382
Qy 353 EHVQKNEVLYIKFLIKYAWYKAPSOYKIREERRLLEAGYQSTTVGAPLVVYI 412
Db 383 KRIGLNEVLAAMDYKCAQVSCFQVQVAVRDELDFWFRRAQQLISANMFLINSIPVL 442
Qy 413 ASVVTFSVMTLGFDLTAQAFTVVTENSMTFALKVTPEFSYKSLSEASVAADRFKSLFL 472
Db 443 VVVSFGVSTLGGDLTPARAFTSLSLFVLRPFLMLNITQMNANVNSLRLEVIS 502

Qy 473 MEEVHIKKNPASP-HIKIEMKNATLAWDSSHSIIQNSPKLTPEKMKDKKRASRKKKEVR 531
Db 503 TEERVLNLPPIEPGQPAISIRNGYFSDS----- 532
Qy 532 QLORTEHOAVLAROKGHLLLDSDERSPEEBEGKTHLGLRLQRLHSLIDLEIQECKLV 591
Db 533-----KADRP-----TLSNINLIDPLGSIV 552
Qy 592 GICGSVSGKTSLSIALIQOM-TLLEGSIAISTFAYVAQAMILNATLRDNLTFCKEYD 650
Db 553 AAVSGTEGKTSLSIAMGELPARSDATVYLRGSVAVVPQVSWIFANVADNLLFGAPFD 612
Qy 651 EERYNVLNSCCRPDLATIPSSDLTEIGRGANLSGGQORSLARALYSDBRSIYLLD 710
Db 613 QEKTERVIDYALOHDELPLPGDGLTEIGRGVNISSGQORVSMARAVYNSDVCILDE 672
Qy 711 PLSDALHVGNNHIFNSAIRKHLKSKTVLFYTHOLOYLVDCEVIFPKEGCITERGTHEEL 770
Db 673 PLSDALHVGQGVFEKCIKRELQOTTRVLTNQLHFLSQVDKTLVHEGTVKEGTYEEL 732
Qy 771 MNLNGDYATIFNNL-----LLGETPVEINSKKEKTSQSKQDKPKTGSIKKERA 822
Db 733 CHSGPLFPRIMEAGKVEDYSEENGAEVHQTSVKFEVENGANNLQDKGIEFKNSKEGNS 792
Qy 823 VKREBQVIOLEKKGQGVPMVSYGYVIOAGGRLAFVIMALPMLNVGSTARFTMWLSY 882
Db 793 V-----LVKREBERGVSWKLEKRYQNALGAMVMMVILCYLVLYOVERVSSITWLSE 846
Qy 883 WIKGSGNTVTYRGNETSVSDSKDNPHMOYASIALSAWMLILKAIQGVVFKGTLR 942
Db 847 WIDSG---TPKHG-----PLFYNIYALLSFGVSYVTILSYMLNLSLY 889
Qy 943 ASSRLDELFRILRSMPKFEFTTPGRLILNRSKMDDEVDRVLPQAEMLIGNVILLVF 1002
Db 890 AAKKMDAMGLSLRAPMVEFQTNPLGRILINRAKMDGIDIRVAVFVNMFGSIQLLS 949
Qy 1003 CVGMINGVPPWFLVAVGPLVILFVSLHIVSRVILRELRKDNTTOSPELHSSIOGLA 1062
Db 950 TVLLIGIVSTLSLMAIMPPLVLYVYGAVLYYQNTSREIKRNDSTTRSVVAQFGEALNGLS 1009
Qy 1063 TIHAYKGOEFLHRYOELDDNOAPFELFTCAMRLAVRLDLSIALITTTGLMIYLMHG 1122
Db 1010 SIFAYAYDMAEINGRSDNNIRFTLVNMAANRWLGIRLEVGLGMVMTTASLAWQNG 1069
Qy 1123 QI--PRAYA---GLAISYAVOLGTLPQTVYRLASETEARETSVERINHYIKTLSLEAPAR 1177
Db 1070 KANQQAAYASTWGLLLSYALSTISLAVRLASLAEKNSLNSYBVGNYIEIPS-EAPLV 1128
Qy 1178 IKKAPSPDPQDGEYTFEAKERYRENLPVLYKKVSTFKPEKIGIYVRTSGSKSLG 1237
Db 1129 IENNRRPPGMPSSGSIKIFEDVVLARKRPDLRPLVHLGVSFLLSPMDKGIYGRGAGKSSLL 1188
Qy 1238 MALFLVELSGGCIKIDGVISDGLADLRKSLIIPQPVLFSGVRSNDLPNOTED 1297
Db 1189 NALFLVELTEKRLILDECDIGRFGLMDLRKYVGLIPQAVLFSGVIRNLPDFSEHND 1248
Qy 1298 QIWDALERTHMEKCIADLPKLESEVMENGDNFVSGEROLLICARALLRCKILLIDEAT 1357
Db 1249 DLMESLEHRLKDTIRRNPLGDAEYTEGENFVSQOROLLISARALLRCKILLIDEAT 1308
Qy 1358 AAMDTELDLLIQTIREAFADCTMLTIAHRLHVLGSDRIMVLAQGVVEFDPSPVLSLN 1417
Db 1309 AAVDRTDVLIOKTIREEFKSCMTLIIAHLRLNTIIDCKVVLVDGKVOEFSSPENLSN 1368
Qy 1418 DSSRFYAM 1425
Db 1369 GESSFSKM 1376

RESULT 15
US-09-935-625-26572
; Sequence 26572, Application US/09935625

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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935, 625
NUMBER OF SEQ ID NOS: 3136
SEQ ID NO 26572
LENGTH: 1622
TYPE: PRF
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..1622
OTHER INFORMATION: Ceres Seq. ID no. 3087736
US-09-935-625-26572

Query Match 27.6%; Score 2013.5; DB 5; Length 1622;
Best Local Similarity 34.3%; Pred. No. 7.6e-141;
Matches 476; Conservative 240; Mismatches 501; Indels 171; Gaps 21;

QY 74 EEPKKGHHGSLAKRIRTCQKHQVNDNAGLFSCMTFSLSLAVAKKGLSMDY 133
DB 217 EEPKGG-----NICPRH---ANLFDSTFFSLMNLMLGSKR-PLTEKDV 259
QY 134 WSLKHESSDVNCRRLERLMOEELNEVDPDAASLRVWTFRCRTLLISVCLMTQLAG 193
DB 260 WHLDYMDKTTLMRSFQKSKMDELEKRP-----W-----LLRALNNSLGG 300
QY 194 -----FSGAFKVKHLEKTYQATES---NLOVSLDVLGLLLEIVRSW 234
DB 301 RFWGWGFWKIGNDSCQFVGP-LLLNELKMSQMLNEPAMIGIYIAISFVGVLGVLCE-- 357
QY 235 SLALTNALNRTGVRLNGALITLMAFKKILTKNKEKSL--GELINCSNDGQRMFAAA 292
DB 358 --AQYQNVNRKVGRLSALIAAVERKSLRLTYEGRKKEFGTKTNMTTDAESLQOIQ 415
QY 293 VGSLLAGPVALLIGMYNTIILPTGFLGSAVFILFYPMMEFASRLTAVERRCVATD 352
DB 416 SLTMTMSAPRIIYALVLYLQOLGVAIIIGALPLVLMFIQYIISTOKITKRGLORTD 475
QY 353 ERYQKNEVLTLYIKIMYAVKAFSOSVQKIEERRILIEKAGYFOSITGVAPIVVI 412
DB 476 KRIGLMEVLAAMDYVCYAMENSFOKQVOTVRDELSPFRKAQLLSAFNMFILNSIPV 535
QY 413 ASVYTFSVHNTLGEDTLAQAFTVYVENMTFALKYTPFSVKSLSASAIVDRFKSLFL 472
DB 536 VIVVSGVFSLGDLTPAPAFSTLSLFSVLRPLFPLPMLPITQMVANVNSLNLLEVL 595
QY 473 MEEVHMINKNPASP-HIKIKMNATLAMDSSHSSSIONSPKLTTPMKKDKRASRGKKEVR 531
DB 596 TEERVLLPNPPIEPGPAPISIRNGYPSWD----- 625
QY 532 QLORTEHQAVALADQKGLLLDSDEPSPPEEKEGHHGLRLQRTLSIDLEIOEGKLV 591
DB 626 -----KADRP-----TLNINLIDPLGSLV 645
QY 592 GICGVSQKSTSLISATLQGM-TLLEGSIAISGTFATVAQOANTLNTLDNIIKFEYD 650
DB 646 AAVGSGEGEKTSLISAMIGELPARSDATVTLRGSVAVPQVSWIFNATVRDNLIFGAPD 705
QY 651 EERYNSVNLNCCRPDLAIIPSSDLPEIGERGANLGGGQRORIISIAARVSDRSIYLLD 710
DB 706 QEKTEEVIVDTALQHDLELLPGDLETFIGRGVNISSGQKORVSMARAVTSNSDVCILDE 765
QY 711 PLSALDAHVGNIHNSAIRKHLKSKTVLFTYHOLYLVDCDEVIFMKEGCITERTGTHEEL 770
DB 766 PLSALDAHVGQYVEKCIKRELQGTTRVLTNQLHLFSQVDKILLVHEGVKKEGTIEEL 825
QY 771 MNINGDIATIFNNL-----LLGETPVEINSKKEKTSQKKSQDKGPKTSIKKEKA 822

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DB 826 CHSGPLPRLMENAGKYEDYSEENGAEVHOTSVKPYENGANNLQDKGIEFTKSKSGNS 885
QY 823 VKPEGOLVLOLEEKQGSVPWYGVYIOAGGPLAFLVIMALEMLNVGSTAFSTWMLSY 882
DB 886 V-----LVKREERETGVSKKVLIERQONLGAAMVVMMLVICVLVOVFVSSITWLS 939
QY 883 WIKQSGNTVYTRGNENFSVSDSKMDNPMQYASIVALSAAVMLILKAIRGVFVKQTLR 942
DB 940 WTDGSG---TEKTHG-----PLFYNIVYALLSFGQVSVLLINSYMLIMSLSLY 982
QY 943 ASSRLHDELFRILRSMPKFPDTPGTGRLNREKSGKDEVDVRLPFGAENQIVVILVFF 1002
DB 983 AAKMHDMAMGSLIRAPVVEFQTNPLGRILINREKADMGDDIRYAVFVNMMSGIAOLLS 1042
QY 1003 CVGMIAGVFPWFELVAVGPLVILFSLVLIIVSRVLLIRELKRDLNITQSPFLSHITSSIOGLA 1062
DB 1043 TYLILIGIVSTLSLMAIMPPLVVFYGAVLYQNTSREIKRMDSTIRSVYVQFGALNGLS 1102
QY 1063 TIHAYNKQGEFLHRYQELLDNOAPFELFTCAMRWLAVRDLISALITTTGLMIVLMHG 1122
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 09:13:40 ; Search time 92.45 Seconds
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Title: US-09-528-031-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4775.4	98.5	4781	2	US-09-001-273-1 Sequence 1, App11
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4	511.2	10.5	5011	1	US-08-463-092B-3 Sequence 3, App11
5	511.2	10.5	5011	2	US-08-462-109A-3 Sequence 3, App11
6	511.2	10.5	5011	2	US-08-460-907B-3 Sequence 3, App11
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ALIGNMENTS

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US-09-061-400-1
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; Patent No. 6077936
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,400
; FILING DATE: 16-APRIL-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNT-056CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4847 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116..4426
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Matches 4847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 4621 TCATCTTAACAAATTTTATTTTGTCTTCTTAATTCACCTCTAAAGGTTTCAGGAAACCGT 4680
QY 4681 TATTTAATTTATTCAGAGGCTTATTAATGAACTTATTCAGTCTATCTATATAT 4740
Db 4681 TATTTAATTTATTCAGAGGCTTATTAATGAACTTATTCAGTCTATCTATATAT 4740
QY 4741 AATCTGTACATAGGCTTATTTTACAGTGAATGTAAAGCTTTATTTTATTTTAAAT 4800
Db 4741 AATCTGTACATAGGCTTATTTTACAGTGAATGTAAAGCTTTATTTTATTTTAAAT 4800
QY 4801 AAGCACTGCTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAAT 4847
Db 4801 AAGCACTGCTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAAT 4847

RESULT 2

US-09-001-273-1
Sequence 1, Application US/09001273
Patent No. 5994130
GENERAL INFORMATION:
APPLICANT: SHYUAN, Andrew
TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001,273
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FENTON, Gillian M
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIL-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 2..4360
US-09-001-273-1

Query Match 98.5%; Score 4775.4; DB 2; Length 4781;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4773; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 67 TGAATGGAATCTTACAGTGTGTGAGCCCTGGAACCTTCACCTCAGAGAGATGAGATAT 126
Db 1 TGAATGGAATCTTACAGTGTGTGAGCCCTGGAACCTTCACCTCAGAGAGATGAGATAT 60
QY 127 CGCATAGAGAAAGAT 186
Db 61 CGCATAGAGAAAGAT 120
QY 187 CAGCACTTCTGGGAGCCAGAGAGACCGTGAAGATTTCCAGATTTCCAGAGAGATCCGATT 246
Db 121 CAGCACTTCTGGGAGCCAGAGAGACCGTGAAGATTTCCAGATTTCCAGAGAGATCCGATT 180
QY 247 GGAATGCCAAGATGCCCTTGGAAACAGACCCGAGCCGAGGCGCTCTCTTGAATGCTTC 306
Db 181 GGAATGCCAAGATGCCCTTGGAAACAGACCCGAGCCGAGGCGCTCTCTTGAATGCTTC 240
QY 307 CATGATTTCTCAGCTCAGATTCCTGGATGAGAGCATCCCAAGGAAATACCATCATGG 366
Db 241 CATGATTTCTCAGCTCAGATTCCTGGATGAGAGCATCCCAAGGAAATACCATCATGG 300
QY 367 CTTGAGTGTCTGAAGCCCATCCGACTTGTGCAAAACAGACACCCAGTGGACATATGC 426
Db 301 CTTGAGTGTCTGAAGCCCATCCGACTTGTGCAAAACAGACACCCAGTGGACATATGC 360
QY 427 TGGGCTTTTCTCTGATACATTTTCTGAGCTTTCTGAGCTTTCTGAGCTTTCTGAGCTTT 486
Db 361 TGGGCTTTTCTCTGATACATTTTCTGAGCTTTCTGAGCTTTCTGAGCTTTCTGAGCTTT 420
QY 487 GAAGGGGAGCTCTCAATGGAAGAGCTGTGCTCTGTCCAGACAGAGCTTTCTGAGCT 546
Db 421 GAAGGGGAGCTCTCAATGGAAGAGCTGTGCTCTGTCCAGACAGAGCTTTCTGAGCT 480
QY 547 GAATGTCAGAGAGCTAGAGAGACTGTGGCAAGAGAGCTGAATGAATTTGGCCAGAGCG 606
Db 481 GAATGTCAGAGAGCTAGAGAGACTGTGGCAAGAGAGCTGAATGAATTTGGCCAGAGCG 540
QY 607 TGGTTCCTCTGCAAGAGGTTGTGTGATCTTCTGCGGACACAGGCTCATCTCTCATGCT 666
Db 541 TGGTTCCTCTGCAAGAGGTTGTGTGATCTTCTGCGGACACAGGCTCATCTCTCATGCT 600
QY 667 GTGCTGATGATCACGACAGCTGGCTGCTTCAAGTGAGACAGGCTTCATGTAACACCT 726
Db 601 GTGCTGATGATCACGACAGCTGGCTGCTTCAAGTGAGACAGGCTTCATGTAACACCT 660
QY 727 CTTGAGATATACCCAGGCAAGAGCTTAACCTGCAGTACAGCTTGTGTTAGTCTGGG 786
Db 661 CTTGAGATATACCCAGGCAAGAGCTTAACCTGCAGTACAGCTTGTGTTAGTCTGGG 720
QY 787 CCTGCTCTGAGGAAATGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 846
Db 721 CCTGCTCTGAGGAAATGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 780
QY 847 CGGAACCGGTGTCCGCTTCCGGGGGCGCATCTTAACATGAGGATTTAAAGATCTTTAA 906
Db 781 CGGAACCGGTGTCCGCTTCCGGGGGCGCATCTTAACATGAGGATTTAAAGATCTTTAA 840
QY 907 GTTAAAGAACATTTAAAGAAATCCCTGGGTAGCTCATCAACATTTGCTCCAGACATGG 966
Db 841 GTTAAAGAACATTTAAAGAAATCCCTGGGTAGCTCATCAACATTTGCTCCAGACATGG 900
QY 967 GCAGAGATGTTTGAAGCAGACGCGTGTGAGCCTGCTGCTGAGAGACCCGTTGTTGC 1026
Db 901 GCAGAGATGTTTGAAGCAGACGCGTGTGAGCCTGCTGCTGAGAGACCCGTTGTTGC 960
QY 1027 CATCTTAGCATGATTTTAAATGTAATTAATTTGAGGACCAAGGCTTCGGGATTCAGC 1086
Db 961 CATCTTAGCATGATTTTAAATGTAATTAATTTGAGGACCAAGGCTTCGGGATTCAGC 1020

QY	1087	TGTTTTATCCCTCTTTTATCCAGCAATGATGTTTGCATCCAGGCTCACAGCATATTTCCAG	1146
Db	1021	TGTTTTATCCCTCTTTTATCCAGCAATGATGTTTGCATCCAGGCTCACAGCATATTTCCAG	1080
QY	1147	GAGAAATGGGTGGCCGCGCCAGGATACAGGTGCCAAGAAATGAAGTTCTTACTTA	1206
Db	1081	GAGAAATGGGTGGCCGCGCCAGGATACAGGTGCCAAGAAATGAAGTTCTTACTTA	1140
QY	1207	CATTAAATTTATCAAAATGATGATCCCTGGGTCAAGCATTTTCTCAGAGTGTTCAGAAAT	1266
Db	1141	CATTAAATTTATCAAAATGATGATCCCTGGGTCAAGCATTTTCTCAGAGTGTTCAGAAAT	1200
QY	1267	CCGCGAGAGAGAGCGTCGATATTGCAAAAACCGGGTACTTCCAGACATCACTGTGGG	1326
Db	1201	CCGCGAGAGAGAGCGTCGATATTGCAAAAACCGGGTACTTCCAGACATCACTGTGGG	1260
QY	1327	TGTGGCTCCCATTTGTGGTGTATTTCCAGCGGGTGAACCTTCCTGTTCATATGACCTT	1386
Db	1261	TGTGGCTCCCATTTGTGGTGTATTTCCAGCGGGTGAACCTTCCTGTTCATATGACCTT	1320
QY	1387	GGGCTTCGATCTGACAGCAGCACAGGCTTTTCACAGTGTGACAGTCTTCAATTCATGAC	1446
Db	1321	GGGCTTCGATCTGACAGCAGCACAGGCTTTTCACAGTGTGACAGTCTTCAATTCATGAC	1380
QY	1447	TTTTGCTTTAAGAGTAAACCCGTTTTCAGTAAAGTCCCTCTAGAAAGCCTCAGTGGCT	1506
Db	1381	TTTTGCTTTAAGAGTAAACCCGTTTTCAGTAAAGTCCCTCTAGAAAGCCTCAGTGGCT	1440
QY	1507	TGACAGATTTAAGAGTTGTTTCTAATGGAAGAGTTCACATGATTAAGAAACAACAGC	1566
Db	1441	TGACAGATTTAAGAGTTGTTTCTAATGGAAGAGTTCACATGATTAAGAAACAACAGC	1500
QY	1567	CAGTCTCACATCAAGTATAGATGA AAAATGCCACCTTGGCATGGACTCTCCCACTC	1626
Db	1501	CAGTCTCACATCAAGTATAGATGA AAAATGCCACCTTGGCATGGACTCTCCCACTC	1560
QY	1627	CAGTATCCAAATCCGCCCAAGCTGACCCCAAAATGAAAAAGCAGAGAGGCTCCAG	1686
Db	1561	CAGTATCCAAATCCGCCCAAGCTGACCCCAAAATGAAAAAGCAGAGAGGCTCCAG	1620
QY	1687	GGCGAAGAAAGAGAGGTGAGGCAGCTGCAGCGCACCTAGCATAGGCGGTCTGGGAGA	1746
Db	1621	GGCGAAGAAAGAGAGGTGAGGCAGCTGCAGCGCACCTAGCATAGGCGGTCTGGGAGA	1680
QY	1747	GCACAAAGGCGACCTCCTCTGTGGACAGTACAGAGGCGCCAGTCCCGAAGAGAAAGG	1806
Db	1681	GCACAAAGGCGACCTCCTCTGTGGACAGTACAGAGGCGCCAGTCCCGAAGAGAAAGG	1740
QY	1807	CAAGCAGATCCACCTGGGCGACCTGGCGCTTACAGAGGACACTGCACACATCTGATCGGA	1866
Db	1741	CAAGCAGATCCACCTGGGCGACCTGGCGCTTACAGAGGACACTGCACACATCTGATCGGA	1800
QY	1867	GATCCAGAGAGGTAACCTGGTTGGAATCTGCGGCGAGTGTGGGAAGTGGAAAACTCTCT	1926
Db	1801	GATCCAGAGAGGTAACCTGGTTGGAATCTGCGGCGAGTGTGGGAAGTGGAAAACTCTCT	1860
QY	1927	CATTTCAGCCATTTTAGCCAGCATGACGCTTTTAAAGGCGACAGCATTTGCAATCACTGGAC	1986
Db	1861	CATTTCAGCCATTTTAGCCAGCATGACGCTTTTAAAGGCGACAGCATTTGCAATCACTGGAC	1920
QY	1987	CTTTCGCTTATGTGGCCAGCAGAGGCTGTGATCTCTCAATGCTTACTGTGAGAGCAACATCT	2046
Db	1921	CTTTCGCTTATGTGGCCAGCAGAGGCTGTGATCTCTCAATGCTTACTGTGAGAGCAACATCT	1980
QY	2047	GTTTGGGAAGATATTGATGAAGAAAGATACAACCTGCGCGAAGACACTCTGCGTAG	2106
Db	1981	GTTTGGGAAGATATTGATGAAGAAAGATACAACCTGCGCGAAGACACTCTGCGTAG	2040
QY	2107	GCTGACCTTGGCCATCTTCCAGCAGCGACCTGACGAGATTTGGAGAGCGAGAGCCAA	2166
Db	2041	GCTGACCTTGGCCATCTTCCAGCAGCGACCTGACGAGATTTGGAGAGCGAGAGCCAA	2100

QY	2167	CCTGAGCGGTGGCGAGCGGCCAGAGAGTCAgCCTTGGCCGGCCCTGTATAGTACAGAGG	2228
Db	2101	CCTGAGCGGTGGCGAGCGGCCAGAGAGTCAgCCTTGGCCGGCCCTGTATAGTACAGAGG	2160
QY	2227	CATCTACATCCTGGACGACCCCTCGAGTGGCTTATAGTATGGCCATGTTGGGCAACATATTT	2286
Db	2161	CATCTACATCCTGGACGACCCCTCGAGTGGCTTATAGTATGGCCATGTTGGGCAACATATTT	2220
QY	2287	CAATAGTGTCTATCCGGAAACAATCTCAAGTTCAGACAGTTCCTGTTTGTATACCAACATTT	2346
Db	2221	CAATAGTGTCTATCCGGAAACAATCTCAAGTTCAGACAGTTCCTGTTTGTATACCAACATTT	2280
QY	2347	ACAGTACCTGGTGTACGTTGTATGAAGTATCTTTCATGAAGAAGGGCTGTATTACGGAAG	2406
Db	2281	ACAGTACCTGGTGTACGTTGTATGAAGTATCTTTCATGAAGAAGGGCTGTATTACGGAAG	2340
QY	2407	AGGCACCCATGAGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTAAATAACT	2466
Db	2341	AGGCACCCATGAGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTAAATAACT	2400
QY	2467	GTTGGTGGAGACAGACCCGGCAGTGGAGATCAATTCAAAAAAGGAACAGAGGTTCACA	2566
Db	2401	GTTGGTGGAGAGACACCCGGCAGTGGAGATCAATTCAAAAAAGGAACAGAGGTTCACA	2460
QY	2527	GAAAGAATCACAAACACAAGGGGTCTTAAACAGGATCAATTAAGAAGAAAAAGCAGTAAA	2586
Db	2461	GAAAGAATCACAAACACAAGGGGTCTTAAACAGGATCAATTAAGAAGAAAAAGCAGTAAA	2520
QY	2587	GCCAGAGGAAGGCGACTTGTGCAAGCTGCAAGAGAAAGGGCAGGGTCAGTCCCTGCTC	2646
Db	2521	GCCAGAGGAAGGCGCGCTTGTGCAAGCTGCAAGAGAAAGGGCAGGGTCAGTCCCTGCTC	2580
QY	2647	AGTATATGTTGTCTACATTCAGAGCTGCTGGGGGGCCCTTGGCATTCGTTGATATATATGC	2706
Db	2581	AGTATATGTTGTCTACATTCAGAGCTGCTGGGGGGCCCTTGGCATTCGTTGATATATATGC	2640
QY	2707	CCTTTTCATGCTGTAATATAGCAGACACCGCTTTCACACCTGTTGGTTGAGTTACTGGAT	2766
Db	2641	CCTTTTCATGCTGTAATATAGCAGACACCGCTTTCACACCTGTTGGTTGAGTTACTGGAT	2700
QY	2767	CAAGCAAGGAAGCGGGAACACCACTGTGACTGAGGGAACGAGACCTGGTGTAGTGACAG	2826
Db	2701	CAAGCAAGGAAGCGGGAACACCACTGTGACTGAGGGAACGAGACCTGGTGTAGTGACAG	2760
QY	2827	CATGAAGAACAATCCTCATATGCAAGTACATATGCAACATCTACGCGCTCTCCATGAGGCACT	2886
Db	2761	CATGAAGAACAATCCTCATATGCAAGTACATATGCAACATCTACGCGCTCTCCATGAGGCACT	2820
QY	2887	CATGCTGATCCTTGAAGACCAATTCGAGAGAGTGTCTTTCGAAGGGCACGCTGCAGACTTC	2946
Db	2821	CATGCTGATCCTTGAAGACCAATTCGAGAGAGTGTCTTTCGAAGGGCACGCTGCAGACTTC	2880
QY	2947	CTCCCGGCTGCATGACGAGCTTTTTCGGAAGAGATCCTTCGAAGCCCTATGAAGTTTTTGA	3006
Db	2881	CTCCCGGCTGCATGACGAGCTTTTTCGGAAGAGATCCTTCGAAGCCCTATGAAGTTTTTGA	2940
QY	3007	CACGACCCCCCAAGGAGGAGATTCTCAACAGGTTTTCCAAAGACATGATGAAGTTGAGACT	3066
Db	2941	CACGACCCCCCAAGGAGGAGATTCTCAACAGGTTTTCCAAAGACATGATGAAGTTGAGACT	3000
QY	3067	GGCGGCTCCGTTCCAGGCGAGATGTTTCATATCCAGAAAGTATACCTGAGTGTCTTCTGAGT	3126
Db	3001	GGCGGCTCCGTTCCAGGCGAGATGTTTCATATCCAGAAAGTATACCTGAGTGTCTTCTGAGT	3060
QY	3127	GGGAATGATGCAAGAGTCTTCCCGTGGTTCTTGTGGCAGTGGGGCCCTTGTCTATCCTT	3186
Db	3061	GGGAATGATGCAAGAGTCTTCCCGTGGTTCTTGTGGCAGTGGGGCCCTTGTCTATCCTT	3120
QY	3187	CTTTTCAGTCTGCAATTTGTCTCCAGAGGTTCCGATGAGGAGCTGAAGCCCTGGAGCAA	3246
Db	3121	CTTTTCAGTCTGCAATTTGTCTCCAGAGGTTCCGATGAGGAGCTGAAGCCCTGGAGCAA	3180
QY	3247	TATACGCGATACATCTTCTCTCCACATTCACGTCCAGACATACAGGGCCCTTGGCACCAT	3306

FEATURE:
NAME/KEY: CDS
LOCATION: 2..4360
US-08-843-459A-1

Query Match 98.5%; Score 4775.4; DB 4; Length 4781;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4773; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 67 TGATGTGAACTAAGCTGTGTGAGCCCTGAACTCCACTCAGAGAAGATGAAGATAT 126
DB 1 TGATGTGAACTAAGCTGTGTGAGCCCTGAACTCCACTCAGAGAAGATGAAGATAT 60
QY 127 CGACATGTGAAAAAGATATATCATCCCAATGCTGGGTATATGAAGTGTGAGGGAGAAC 186
DB 61 CGACATGTGAAAAAGATATATCATCCCAATGCTGGGTATATGAAGTGTGAGGGAGAAC 120
QY 187 CAGCACTTGTGGACGACAGACAGACCGTGAAGATTCCAGTTGAGAGAACTGACCGTT 246
DB 121 CAGCACTTGTGGACGACAGACAGACCGTGAAGATTCCAGTTGAGAGAACTGACCGTT 180
QY 247 GGAATGCCAAGATGCTTGTGAACACAGACGACGACGACGCTCTCTTGTATGCTC 306
DB 181 GGAATGCCAAGATGCTTGTGAACACAGACGACGACGACGACGCTCTCTTGTATGCTC 240
QY 307 CAGCACTTGTGAGCTGTGATCTGTGATGTGAGAGCATCCCAAGGAAATGCCATCATG 366
DB 241 CAGCACTTGTGAGCTGTGATCTGTGATGTGAGAGCATCCCAAGGAAATGCCATCATG 300
QY 367 CTTGAGTGTCTGTGAAGCCATCCGACTACTTGTGAACACAGACGACGACGATGAC 426
DB 301 CTTGAGTGTCTGTGAAGCCATCCGACTACTTGTGAACACAGACGACGACGATGAC 360
QY 427 TGGGCTTTTTCCTGTATGACTTTTTCGTGGCTTTCTCTGTGGCCCGTGTGGCCCAA 486
DB 361 TGGGCTTTTTCCTGTATGACTTTTTCGTGGCTTTCTCTGTGGCCCGTGTGGCCCAA 420
QY 487 GAAAGGGGAGCTCTCATGTGAAGACGTTGTCTCTCTCAAGACAGATCTTGTGACGT 546
DB 421 GAAAGGGGAGCTCTCATGTGAAGACGTTGTCTCTCTCAAGACAGATCTTGTGACGT 480
QY 547 GAACTGAGAGACTAGAGAGACTGTGGCAAGAAAGACTGAATGAATTTGGGCCAGACG 606
DB 481 GAACTGAGAGACTAGAGAGACTGTGGCAAGAAAGACTGAATGAATTTGGGCCAGACG 540
QY 607 TGCCTTCCTCGAAGGGTGTGTGATCTTCTGTGCCACCAAGGCTCATCTGTCCATGCT 666
DB 541 TGCCTTCCTCGAAGGGTGTGTGATCTTCTGTGCCACCAAGGCTCATCTGTCCATGCT 600
QY 667 GTGCTGTATGATCAGCAGAGTGTGTGCTCAGTGAACAGCCCTTCATGTGAAACACT 726
DB 601 GTGCTGTATGATCAGCAGAGTGTGTGCTCAGTGAACAGCCCTTCATGTGAAACACT 660
QY 727 CTTGAGATATACCAGGCAACAGAGTCTAACCTGTCAAGTATAGCTTGTGTAGTGGGG 786
DB 661 CTTGAGATATACCAGGCAACAGAGTCTAACCTGTCAAGTATAGCTTGTGTAGTGGGG 720
QY 787 CCTTCCTCTAGCGAAATGCTGTGCGCTTGTGTGCTGCACTGACATTTGGGCAATTGAATTA 846
DB 721 CCTTCCTCTAGCGAAATGCTGTGCGCTTGTGTGCTGCACTGACATTTGGGCAATTGAATTA 780
QY 847 CGGAACGGGTGCGGCTTGTGGGGGGGCAATCCTAACCATGGCATTTAAGAAGATCCTTAA 906
DB 781 CGGAACGGGTGCGGCTTGTGGGGGGGCAATCCTAACCATGGCATTTAAGAAGATCCTTAA 840
QY 907 GTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCAACGATGG 966
DB 841 GTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCAACGATGG 900
QY 967 GCAGAGAAATTTGAGGACAGACCGCTTGGCAGCTGTCTGCTGAGAGACCCGTTGTTGC 1026
DB 901 GCAGAGAAATTTGAGGACAGACCGCTTGGCAGCTGTCTGCTGAGAGACCCGTTGTTGC 960

QY 1027 CATCTTAGCATGATTTATATATATATATCTGTGGACCAACAGGCTTCTGGGATCAGC 1086
DB 961 CATCTTAGCATGATTTATATATATATATATCTGTGGACCAACAGGCTTCTGGGATCAGC 1020
QY 1087 TGTTTTATCTCTTTTACCAGCAATGATTTTGCATCAGGGCTCACAGCATATTTAG 1146
DB 1021 TGTTTTATCTCTTTTACCAGCAATGATTTTGCATCAGGGCTCACAGCATATTTAG 1080
QY 1147 GAGAAATGCGTGGCCGCGACGATGAACGTTCCAGAAATGATGAAGTTCTTACTTA 1206
DB 1081 GAGAAATGCGTGGCCGCGACGATGAACGTTCCAGAAATGATGAAGTTCTTACTTA 1140
QY 1207 CATTTAATTTTCAAAATGTATGCTGTGGTCAAAAGCATTTTCTCAGAGTGTCCAAAT 1266
DB 1141 CATTTAATTTTCAAAATGTATGCTGTGGTCAAAAGCATTTTCTCAGAGTGTCCAAAT 1200
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DB 1201 CCGGAGAGAGAGGCGTGGATATGAAAAACCGGGTACTTCCAGAGCATCAGTGGG 1260
QY 1327 TGTGGTCCCATTTGTGTGTGATTTGCCAGGCTGGTGAACCTTCTGTTCATATGACCT 1386
DB 1261 TGTGGTCCCATTTGTGTGTGATTTGCCAGGCTGGTGAACCTTCTGTTCATATGACCT 1320
QY 1387 GGGCTTGATGTGACAGCAGACAGGCTTTCACAGTGGTGAAGTCTTCAATTCATGAC 1446
DB 1321 GGGCTTGATGTGACAGCAGACAGGCTTTCACAGTGGTGAAGTCTTCAATTCATGAC 1380
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DB 1381 TTTTGTGTAAGATTAACACCGTTTTCAGTAAAGTCCCTCCAGAGGCTCAGTGGCT 1440
QY 1507 TGACAGATTTAAGAGTTTGTCTTAATGGAAGAGTTTCATATGAAGAAACAAACAGC 1566
DB 1441 TGACAGATTTAAGAGTTTGTCTTAATGGAAGAGTTTCATATGAAGAAACAAACAGC 1500
QY 1567 CAGTCTCAGATCAAGATTAAGATGAAGAAATGCCACCTTGGCATAGGACTCTCCCATC 1626
DB 1501 CAGTCTCAGATCAAGATTAAGATGAAGAAATGCCACCTTGGCATAGGACTCTCCCATC 1560
QY 1627 CAGTATCAGAACTGCGCAAGCTGACGCCCAATATGAAGAAAGAGGGCTTCAG 1686
DB 1561 CAGTATCAGAACTGCGCAAGCTGACGCCCAATATGAAGAAAGAGGGCTTCAG 1620
QY 1687 GGGCAAGAAAGAGAGGTGAGGACGCTGACAGCGCATGAGCATGAGCGGTGTGGCAGA 1746
DB 1621 GGGCAAGAAAGAGAGGTGAGGACGCTGACAGCGCATGAGCATGAGCGGTGTGGCAGA 1680
QY 1747 GCAGAAAGGCACTCTCTCGAGACATGAGACGCGGCCCATGCCAAAGAGAAAGG 1806
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QY 1807 CAAGCATCATCAGCTGGGCGCACTGCGCTTTCAGAGGACATGTGACAGCATGATGGA 1866
DB 1741 CAAGCATCATCAGCTGGGCGCACTGCGCTTTCAGAGGACATGTGACAGCATGATGGA 1800
QY 1867 GATCCAAAGAGGTAACGTGTTGAATCTGCGGACGTGTGGAGTGGAAAAACCTCTCT 1926
DB 1801 GATCCAAAGAGGTAACGTGTTGAATCTGCGGACGTGTGGAGTGGAAAAACCTCTCT 1860
QY 1927 CATTTAGCATTTTAAAGCCAGATGAGCGCTTTCAGAGGCGAGCTTGCATCATGTGAA 1986
DB 1861 CATTTAGCATTTTAAAGCCAGATGAGCGCTTTCAGAGGCGAGCTTGCATCATGTGAA 1920
QY 1987 CTTGCTTATGTGGCCAGAGGCTGTGATCTTCAATGCTACTGTGAGAGCAACATCTCT 2046
DB 1921 CTTGCTTATGTGGCCAGAGGCTGTGATCTTCAATGCTACTGTGAGAGCAACATCTCT 1980
QY 2047 GTTTGGAGAGAAATATATGATGAAGAAATCAACTCTGTGTGTAACAGCTGTGCTGAG 2106
DB 1981 GTTTGGAGAGAAATATATGATGAAGAAATCAACTCTGTGTGTAACAGCTGTGCTGAG 2040

QY	2107	GTGTGACCTGGSCAATTCCTTCCACAGCACGACCTGACGGAAATTGGAAACGAGAGACCA	2166
Db	2041	GCCTTGACCTGGCCATTCCTCCACAGCACGACCTGACGGAAATTGGAAACGAGAGACCA	2100
QY	2167	CCGACACGGTGGGACAGGGCCAGAGGAATCACCTTGCCGGGGCCCTGTATATGTGACAGAG	2226
Db	2101	CCGACACGGTGGGACAGGGCCAGAGGATCACCTTGCCGGGGCCCTGTATATGTGACAGAG	2160
QY	2227	CATCTACATCTTGAGACGACCCCTCAGTGGCTTAGATGCCCATGTGGGCAACCATCTT	2286
Db	2161	CATCTACATCTTGAGAGACCCCTCAGTGGCTTAGATGCCCATGTGGGCAACCATCTT	2220
QY	2287	CATATGCTATTCGGGAACATCTCAAGTCCAAAGACAGTTCTGTTTGTATACCCAGCT	2346
Db	2221	CATATGCTATTCGGGAACATCTCAAGTCCAAAGACAGTTCTGTTTGTATACCCAGCT	2280
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Db	2281	ACAGTACCTGGTGGACTGTGATGAAGATCTCATGAAGAGGGCTGTATACGGAAG	2340
QY	2407	AGGACCCATGAGAACTGATGAATTTAAATGGTGCATATCTAACATTTTAAATACCT	2466
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QY	2467	GTTGCTGGAGAGACACCCGCACTGAGATCAATTCAAAAAGGAACACAGTGGTTACA	2526
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QY	2527	GAAAGATGCACAAAGAAAGGTCCTAAACAGGATCAATAAAGGAATAAACAGCTTAA	2586
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QY	2587	GCCAGAGAAAGGACAGCTTGAGAGTGGAAAGAAAGGACAGGTTCACTGGCCCTGTC	2646
Db	2521	GCCAGAGAAAGGACAGCTTGAGAGTGGAAAGAAAGGACAGGTTCACTGGCCCTGTC	2580
QY	2647	AGTATATGCTGTACATCCAGGCTCTGGGGGCCCTTGCGCATTCCTGGTTATATAGC	2706
Db	2581	AGTATATGCTGTACATCCAGGCTCTGGGGGCCCTTGCGCATTCCTGGTTATATAGC	2640
QY	2707	CCCTTTCATGCTGAATGTAGTGAAGACACGCGCTTACACACCTGGTGGTTAGTTACGAT	2766
Db	2641	CCCTTTCATGCTGAATGTAGTGAAGACACGCGCTTACACACCTGGTGGTTAGTTACGAT	2700
QY	2767	CAAGCAAGAAAGCGGGAACACCACTGTGACTCGAGGAAACGAACCTCGGTGATGCAG	2826
Db	2701	CAAGCAAGAAAGCGGGAACACCACTGTGACTCGAGGAAACGAACCTCGGTGATGCAG	2760
QY	2827	CATGAAGCAATCTCTCATATGCACTACTATAGCCAGCATCTACCCCTCTCATAGGCAGT	2886
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QY	2887	CATGCTGATCTCGAAAGCCATTCGAGAGATGTGCTTGTCAAGGCAACGCTGGAGCTTC	2946
Db	2821	CATGCTGATCTCGAAAGCCATTCGAGAGATGTGCTTGTCAAGGCAACGCTGGAGCTTC	2880
QY	2947	CTCCGGGCTGCATGACGAGACTTTTCCGAAGGATCTTTCGAAGCCCTATGAAGTTTTTGA	3006
Db	2881	CTCCGGGCTGCATGACGAGACTTTTCCGAAGGATCTTTCGAAGCCCTATGAAGTTTTTGA	2940
QY	3007	CACGACCCCCACAGGGAGGATTCACACAGTTTTTCCAAAGACATGAGTGAAGTTGACGT	3066
Db	2941	CACGACCCCCACAGGGAGGATTCACACAGTTTTTCCAAAGACATGAGTGAAGTTGACGT	3000
QY	3067	GGGGGTGGCGGCTTCACGGGCGGAGATGTTCATCCAGAACGTTATCTCGTGTCTTCGTGT	3126
Db	3001	GGGGGTGGCGGCTTCACGGGCGGAGATGTTCATCCAGAACGTTATCTCGTGTCTTCGTGT	3060
QY	3127	GGGAATGATCCGAGAGAGTTTCCCGGTGATCTCTTGGGAGAGTGGGCGCCCTGTCAATCT	3186
Db	3061	GGGAATGATCCGAGAGAGTTTCCCGGTGATCTCTTGGGAGAGTGGGCGCCCTGTCAATCT	3120
QY	3187	CTTTTCAGTCTGCACATGTCTCCAGGGTCTGATTTGGAGAGCTGAAGCTCTGCAGCA	3246

Db	3121	CTTTTCAGTCCGACATATGTCCTCAGGGTCGTGATTCGGAGCTGAACGCTCTGGACAA	3180
Qy	3247	TATCAGCAGTCACCTTTCTCTCTCCACATCAGCTCCAGCATACAGGCTTTGCCACAT	3306
Db	3181	TATCAGCAGAGTCACCTTTCTCTCTCCACATCAGCTCAGCATACAGGCTTTGCCACAT	3240
Qy	3307	CCAGCCCTACAAATAAAGGGCAGAGTTTCTGCACAGATTCACAGGAGCTCTGGATGACAA	3366
Db	3241	CCAGCCCTACAAATAAAGGGCAGAGTTTCTGCACAAATACAGAGCTCTCTGATGACAA	3300
Qy	3367	CCAGCTCTCTTTTTTTTTTTTGTACGTGCGATGCGGTGGCTGTGCGGCTGGACCT	3426
Db	3301	CCAGCTCTCTTTTTTTTTTTTGTACGTGCGATGCGGTGGCTGTGCGGCTGGACCT	3360
Qy	3427	CATCAGCATTCGCTCATCACCACCAAGGGGCTGATGTCGTTCTTATGACAGGGCAGAT	3486
Db	3361	CATCAGCATTCGCTCATCACCACCAAGGGGCTGATGTCGTTCTTATGACAGGGCAGAT	3420
Qy	3487	TCCCCACACCTATCGGGGTCCGACATCTTTATGCTGTCCAGTTACGGGGCTGTGCA	3546
Db	3421	TCCCCACACCTATCGGGGTCTCGGCATCTTTATGCTGTCCAGTTACGGGGCTGTGCA	3480
Qy	3547	GTTTACGCTCAGACTGCGATCTGAGACAGAGCTGATTCACCTCGGTGAGAGGATCAA	3606
Db	3481	GTTTACGCTCAGACTGCGATCTGAGACAGAGCTGATTCACCTCGGTGAGAGGATCAA	3540
Qy	3607	TCACACATTTAAGCTCGTCGCTTTGGAAGCACTGCGACAAATTAAGAACAAAGGCTCCTC	3666
Db	3541	TCACACATTTAAGCTCTGTCTTTGGAAGCACTGCGACAAATTAAGAACAAAGGCTCCTC	3600
Qy	3667	CCCTGACTGGCCCCAGGAGGGAAGGTGACCTTTGAAACGACAGATGAGGTACCGAGA	3726
Db	3601	CCCTGACTGGCCCCAGGAGGGAAGGTGACCTTTGAAACGACAGATGAGGTACCGAGA	3660
Qy	3727	AAACCTCCCTCTGCTCTCTAAAGAAATGTCCTTACGATCAAACTTAAAGAGAAATGG	3786
Db	3661	AAACCTCCCTCTCTCTCTTAAAGAAATGTCCTTACGATCAAACTTAAAGAGAAATGG	3720
Qy	3787	CATTGTGGGGCGGACAGATCAGGAAAGTCGCTGGGGATGGGCCCTTCCCTGCTGAT	3846
Db	3721	CATTGTGGGGCGGACAGATCAGGAAAGTCGCTGGGGATGGGCCCTTCCCTGCTGAT	3780
Qy	3847	GGAATTTCTGAGAGCTGCATCAAGATTGATGAGTGAATCACTGATATTGGCCCTTGC	3906
Db	3781	GGAATTTCTGAGAGCTGCATCAAGATTGATGAGTGAATCACTGATATTGGCCCTTGC	3840
Qy	3907	CGACCTCGGAAGCAAACTCTCATATTCCTCTCAAGAGCCGGGTGCTCATGAGCACATG	3966
Db	3841	CGACCTCGGAAGCAAACTCTCTCATATTCCTCTCAAGAGCCGGGTGCTCATGAGCACATG	3900
Qy	3967	CAGATCAAAATTTGGACCCCTTTCACCAAGTACACTGAAGCACGATTTGGATGCCCTTGA	4026
Db	3901	CAGATCAAAATTTGGACCCCTTTCACCAAGTACACTGAAGCACGATTTGGATGCCCTTGA	3960
Qy	4027	GAGAGCACACATGAAANAAGTTATTCCTGACTACTCTGAAACTTGAATCTGAAGGAT	4086
Db	3961	GAGAGCACACATGAAANAAGTTATTCCTGACTACTCTGAAACTTGAATCTGAAGGAT	4020
Qy	4087	GGAGAAATGGGGATAACTTCTCAGTGGGGGAAGGCAAGCTTGTGTGCTATAGTAAGCCT	4146
Db	4021	GGAGAAATGGGGATAACTTCTCAGTGGGGGAAGGCAAGCTTGTGTGCTATAGTAAGCCT	4080
Qy	4147	GCTCCGCACCTGTAGATTCTGATTTTATGATGAGCCACAGCTGCGATGACACAGAGAC	4206
Db	4081	GCTCCGCACACGTAAAGATTCTGATTTTATGATGAGCCACAGCTGCGATGACACAGAGAC	4140
Qy	4207	AGACTTATTTGATTAACAAGACCAATCGGAGAGCATTTTGACAGCTGTACCATGCTGACAT	4266
Db	4141	AGACTTATTTGATTAACAAGACCAATCGGAGAGCATTTTGACAGCTGTACCATGCTGACAT	4200
Qy	4267	TGCCCATTCGCTGACACGGTTTATAGCTCCGATAGGATTTATGTGTGTGCCACAGGACAA	4326

[illegible]

RESULT 4
 US-08-463-092B-3
 Sequence 3, Application US/08463092B
 Patent No. 576880
 GENERAL INFORMATION:
 APPLICANT: Cole, Susan P.C.
 APPLICANT: Deeley, Roger G.
 TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
 TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: PARTO RESEARCH & DEVELOPMENT INNOVATIONS
 STREET: Queen's University at Kingston
 CITY: Kingston
 STATE: Ontario
 COUNTRY: CANADA
 ZIP: K7L 3N6
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,092B
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/966,923
 FILING DATE: 27-OCT-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/029,340
 FILING DATE: 8-MAR-1993
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/141,893
 FILING DATE: 26-OCT-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/407,207
 FILING DATE: 20-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Steeg, Carol Miernicki
 REGISTRATION NUMBER: 39,539
 REFERENCE/DOCKET NUMBER: Q1546
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (613) 545-2342
 TELEFAX: (613) 545-6853
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5011 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 196..4788
 US-08-463-092B-3

[illegible]

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QY 2465 CTGTTGCTGGAGACACCCGCACTT---GAGATCAATTCAAAAAGAAACAGTGGT 2521
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QY 2522 TCACAGAAAGAGTACAGACAGG-----GTCTTAAACAGCATCAATAAGAAAG 2573
Db 2860 CCAGGGAAGGAGAACCAATGGAATGCAATGCTGTGTGACGACAGTGCAGGGAAG 2919
QY 2574 AAAAGCAGTAAAGCCAGAGAGAGGAGCTGTGACAGCTG----- 2615
Db 2920 CACTGCGAGACACAGCTAGAGAGCTCTCTCTCTATAGTGGGACATACAGACGACAC 2979
QY 2616 AAGAGAAAGGAGAGGTTCACTGCTGCTGATATATGATGTCTACATCCAGGCTGTG 2675
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QY 2676 GGGG-----CCCTTGGCATTCCTGTATTTATGCCCCCTTTTCACTGATGAGGC 2728
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QY 2729 AGCACCGCTTACAGACCTGTGTGTTAGTTACTGATCAAGCAAGAGAGGAGACAC 2788
Db 3100 GCCATCGAGCTTCTCATCTCTCTCTCAGCATCTTCTTTCATGTGTAACTGTC 3159
QY 2789 ACTGTGACT-----CGAGGAGAGAGACCTGCTGAGTACAGATCAAGACATCT 2842
Db 3160 GCGCTGGCTTCCAACTATTGTGCTCAGCTGTGACTGATGACCCCATGTGCAAGGACT 3219
QY 2843 CATATGAGAGTACTATGCCAGATCTAGCCCTCTCATGAGCATCTCTGATCTGAAA 2902
Db 3220 CAGAGACACAGAAAGTGGCTGAGCTGATGAGAGCCCTGGGATTTTCAAGAGATC 3279
QY 2903 GCCATTTGAGG-----AGTTGCTTTGTCAAGGAGCAGCTGCGAGCTTCCCGGCTG 2956
Db 3280 GCCGTGTTGGCTACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3339
QY 2957 CATACAGAGCTTTTCCGAGAGATCTTTCGAAAGCCCTATGAATTTTTCACAGACCC 3016
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Db 3460 GAGGTCAATCAAGATGTTTCAAGATGATGATGATGATGATGATGATGATGATG 3519
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Db 3760 TATTATCCCGAGCATGCTGGGCAACAGAGTGGCTGGCTGGCTGGCTGGCTGGCTG 3819
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QY 3497 TATGCGGCTGCGCCATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3556
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Db 4000 GAGCTGAGAA---GGAGCGCTCTGCAAAATCCAGAGAGAGCTTCCGCGCAGAGCTGG 4056
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Db 4057 CCCCAGAGAGGAGAGTGAATTCGGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 4116
QY 3737 CTGCTCTTAAAGAAATATCTTCAAGATCAAACTTAAAGAGAGAGAGAGAGAGAG 3796
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QY 3797 CCGAGAGATCAGGAGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3856
Db 4177 CCGAGAGAGCTGGAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4236
QY 3857 GGAGGCTCATCAAGATGATGAGTGAATCAATGATGATGATGATGATGATGATGATGAT 3916
Db 4237 GAGAGAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4296
QY 3917 AGCAACTCTCTATATCTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3976
Db 4297 TTCAAGATCACATCATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4356
QY 3977 TTGAG 4036
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QY 4037 ATGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4096
Db 4417 CTGAAG 4476
QY 4097 GATACTCTCAGTGGGAG 4156
Db 4477 GAG 4536
QY 4157 TGTAAATCTGATTTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4216
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QY 4277 CTGAG 4336
Db 4657 CTCAACACATCATGAGATTAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4716
QY 4337 TTGACAG 4360
Db 4717 TACGGCGCCCATGAG 4740

RESULT 5
US-08-462-109A-3
Sequence 3, Application us/08462109A
Patent No. 5882875
GENERAL INFORMATION:
APPLICANT: Cole, Susan P. C.
APPLICANT: Dealey, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
MULTIDRUG RESISTANT TUMOR CELLS
NUMBER OF SEQUENCES: 6


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Db 3820 TGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3879
Qy 3497 TATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3556
Db 3880 TTGGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3939
Qy 3557 AGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3616
Db 3940 CGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3999
Qy 3617 AAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3676
Db 4000 GAGACTGAGAA---GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4056
Qy 3677 CCCCAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3736
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Db 4057 CCCCAGTGGGCGGAGTGAATTCGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4116
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Db 4117 TTCTGCTCAGGACATCAATGCTCAGATCAATGAGGAGAGAAAGGCTGCTGCTGCTG 4176
Qy 3797 CGGAGGATCAGGAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3856
Db 4177 CGGAGGAGGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4236
Qy 3857 GGAGCTCCTATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3916
Db 4237 GAAGAGAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4296
Qy 3917 AGCAATCTCTATCTTCTCAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3976
Db 4297 TTCAAGATCAGATCATCTCCAGAGACCTGTTTGTGCTGCTGCTGCTGCTGCTGCTG 4356
Qy 3977 TTGAGCCCTTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4036
Db 4357 CTGAGCCATTCAGCAGTACTGCTGATGATGATGATGATGATGATGATGATGATGATG 4416
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Db 4417 CTGAAGGACTTCTGCTGAGCCCTTCTGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 4476
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Db 4477 GAGAACCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4536
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Qy 4217 ATCAAGAGACATCCGAGAGATTTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4276
Db 4597 ATCCAGGCTCAGATCCGAGAGATTTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4656
Qy 4277 CTGACAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4336
Db 4657 CTCAACACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4716
Qy 4337 TTTGACACCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4360
Db 4717 TACGGGCGCCATGAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4740
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RESULT 8
US-08-461-384B-3
: Sequence 3, Application US/08461384B
: Patent No. 6025473
: GENERAL INFORMATION:
: APPLICANT: Cole, Susan P.C.
: APPLICANT: Dealey, Roger G.
: TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESS: PARTO RESEARCH & DEVELOPMENT INNOVATIONS
: STREET: Queen's University at Kingston
: CITY: Kingston
: STATE: Ontario
: COUNTRY: CANADA
: ZIP: K7L 3N6
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/461,384B
: FILING DATE: 05-JUN-95
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/966,923

QY	3497	TATCGGGCTCCGCAATCTCTATGCTGTCACGTTAAGCGGGCTCTCCAGTTTAAGGTC	3556
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QY	3557	AGACTGGCAATCTGAGACAGAAAGCTCGATTCCACTCGGTGGAGAGAGATCAATCTACATT	3616
Db	3940	CGGATGTCATCTGAATTAAGTAAACCAACATCTGAGGCCGTGGAGGCTCAAGAGATTCA	3999
QY	3617	AAGACTGTCTGCTGGAAAGCAAGCACTGGCACAATTAAGAACAAAGGCTCCCTCCCTGACTGG	3676
Db	4000	GAGACTGTAGAA---GGAGGGGCTCTGGCAAAATCCAGGAGACAGCTCGCCACGACGCTGG	4056
QY	3677	CCCCAGAGGAGAGAGGTGACCTTTTGAGAACGACAGATGAGGTATCCAGAAACCTCCCT	3736
Db	4057	CCCCAGGTGGCCGAGTGGAAATTCGGGAACTACTGCTGCGCTACCGAAGAGCACTGGAC	4116
QY	3737	CTGTCTTAAGAAGATATCTTCACGATCAAACTAAAGAGACATTGGCATTTGTGGGG	3796
Db	4117	TTGCTTCTCAGGACATCAATGTGACAGATCAATGGGGGAGAAAGAGTGGATGCTGGGG	4176
QY	3797	CGGACAGATCAGGAGGAAGTCTCGCTGGGGATGGGCCCTTCCTCGCTGGTGGAGTTATCT	3856
Db	4177	CGGAGCGGAGCTGGGAAGTGTCTCCCTGACCCCTGTATTTCGGATTAACAGATCTGCC	4236
QY	3857	GGAGGCTGACATCAAGATTGATGGAGTGAAGATCACTGATATTGGCCTTGCCGACCTCGA	3916
Db	4237	GAGGAGAGATGATCATCATGATGAGCATCAATCGCCAAAGATGGGCTCTCAGACACTCGCG	4296
QY	3917	AGCAAACTCTCTATCAATTCCTCAAGAGCGGGGTGCTTCAGTGGACATGTCAGATCAAT	3976
Db	4297	TTTCAAGATCAACATCATCTCCCCAGGACCTGTATTGTGTTTGGGGTTCCTCCGAAATGAC	4356
QY	3977	TTGGACCCCTTCAACACGATACACTGGAAGACAGATTTTGGGATGCCCTGGAGAGCACAC	4036
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QY	4037	ATGAAACAATGTATTTGCTCAGCTACCTCTGAAACTTGAATCTGAAGCTATGAGAAATGGG	4096
Db	4417	CTGGAAGACTTTCGTGACGCCCTTCTTGCAAAAGCTAGACCAATGAATGTGCAAGAAAGCGGG	4476
QY	4097	GATPAATCTTCAGTGGGGGGAAGCGCAGCTCTTGTCATAGCTAGAGACCCCTGCTGCCAC	4156
Db	4477	GAGAACTCAGTGTGCGGGGAGCGCCACAGCTTGTGTGGCTAGGCCGGGCCCTGCTGAGAG	4536
QY	4157	TGTAAATTTCTGATTTTAGATGAAGCCACACGCTGCCATGAGACACAGACATTAATG	4216
Db	4537	ACGGAAGTCTTGTGTGGTAGGAGCCACAGGAGAGCCGTGGACCTGGAACAGGACGACCTC	4596
QY	4217	ATTCAAGAGACATTCGGAAGAGATTTTGGACACTGATACCATCTGACCAATTGGCCCATGCG	4276
Db	4597	ATCCAGTCCACATCCGGGACACAGATTCTGAGAGACTGCACCCGTCTCAACATGCCCCACGG	4656
QY	4277	CTGCACACGGTTTCTAGGCTCCGATAGGATTTATGTGCTGGCCAGAGACAGTGGTGGAG	4336
Db	4657	CTCAACACACATCATGAGACTACACAAGGGGTATCTGTTGACAAAGGAAATCCAGAG	4716
QY	4337	TTTGACACCCCATCGGTCTTGG 4360	
Db	4717	TACGGGCCCCATCGAGACTCTCTGG 4740	

US-08-141-893-1
 US-08-141-893-1
 : Sequence 1, Application US/08141893
 : Patent No 548519
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Cole, Susan P.C.
 : APPLICANT: Deesley, Roger G.
 : TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN
 : NUMBER OF SEQUENCES: 2
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: LAHVE & COCKFIELD

```

101 STREET: 60 STATE STREET, SUITE 510
102 CITY: BOSTON
103 STATE: MASSACHUSETTS
104 COUNTRY: USA
105 ZIP: 02109
106
107 COMPUTER READABLE FORM:
108 MEDIUM TYPE: Floppy disk
109 COMPUTER: IBM PC compatible
110 OPERATING SYSTEM: PC-DOS/MS-DOS
111 SOFTWARE: PatentIn Release #1.0, Version #1.25
112
113 CURRENT APPLICATION DATA:
114 APPLICATION NUMBER: US/08/141,893
115 FILING DATE:
116 CLASSIFICATION: 424
117 PRIOR APPLICATION DATA:
118 APPLICATION NUMBER: 07/966,923; 08/029,340
119 FILING DATE: 27-OCT-1992; 8-MAR-1993
120
121 ATTORNEY/AGENT INFORMATION:
122 NAME: DeConti, Giulio A. Jr.
123 REGISTRATION NUMBER: 31,503
124 REFERENCE/DOCKET NUMBER: PQ1-002
125
126 TELECOMMUNICATION INFORMATION:
127 TELEPHONE: (617) 227-7400
128 TELEFAX: (617) 227-5149
129
130 INFORMATION FOR SEQ ID NO: 1:
131 SEQUENCE CHARACTERISTICS:
132 LENGTH: 5011 base pairs
133 TYPE: nucleic acid
134 STRANDEDNESS: single
135 TOPOLOGY: linear
136 MOLECULE TYPE: cDNA
137 FEATURE:
138 NAME/KEY: CDS
139 LOCATION: 196..4788
140
141 OS-08-141-893-1

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Query Match	Similarity	10.4%	Score 506.4	DB 1:	Length 5011
Best Local	Similarity	52.4%	Pred. No. 1.3e-121		
Matches 1364:	Conservative	0:	Mismatches 1181:	Indels	Gaps
QY 1811	CACATTCACCTGGGCGACCTGCGCTTACAGAGAACACTGCACAGCATCATCTGGAGATC	1870			
Db 2142	CACATTCACCTGGGCGCA--GGAGCACCCTCCACACTGAATGGCATCATCCTTCACATC	2199			
QY 1871	CAAGAGGGTAAACTGTGTGGAACTGCGGACGTGTGGGAAGTGAAAAACCTCTCTCATT	1930			
Db 2200	CCCGAAGGTGCTGTGGTGGCCGTGTGGGCCAGTGGCGCTGGGAAAGTTGTCCTGCTC	2259			
QY 1931	TCAGCCATTTTAAGCCAGATGACGCTTCTAGAGGGCAGCATTTGCATCATCTGTAACCTTC	1990			
Db 2260	TCAGCCCTCTTGGCTGGAATGATGATGACAAAGTGGAGGGGACAGTGGCTATCAAGGGCTCCGGT	2319			
QY 1991	GCTTATGTGGCCCAACGAGCCCGTGATGCTCATCTACTCTGAGAGACAACATCCGCTT	2050			
Db 2320	GCTATGTGCCACACACAGCGCTGGAATTCAGAAATGATCTCTCCGAGAAAAACATCCTTTT	2379			
QY 2051	GGGAAGGATATGATGAAGAAAGATACAACTGTGCTATCAACAGCTGCTCGTAGAGCCT	2110			
Db 2380	GGATGTCAAGCTGAGGAACCACTATTATACAGTCCGTGATACACAGGCTGTGCCCTCTCCCA	2439			
QY 2111	GACCTGGCCATTCTTCCAGCAGCAGCACTGACGAGATTGAGAGCAGAGCAACCTGT	2170			
Db 2440	GACCTGGAATTCCTGCCAGTGGGATGAGGACAGAGATTGGGCAAGGAGCGTGAACCTG	2499			
QY 2171	AGCGGTGGGCAAGCCACAGAGATCAGCCTTGGCCGGGCTTGTATATGTACAGAGACATC	2230			
Db 2500	TCTGTGGGACAGAAACACACAGCGCTGAGCCTGGCCCGGCGCTGTACTCCAAACCTGCATT	2559			
QY 2231	TACATTCGAGAGACCCCTCAGTGCCTTAATGTGCCATGTGGGGAACCAACCATCTTCATT	2290			
Db 2560	TACCTTCGTGATGATCCCTCTCACACAGTGTGATGGCCCATGTGGGAAACACATCTTTGAA	2619			

QY	2291	AAGGCTAT-----CCGGAAACATCTCAACTCCAAAGACAGTTCTGTTGTTATCCACCAG	2344
Db	2620	AATGTATTGTGGCCCCCAAGGGGATGTCTGAATAACAAAGCGGGATCTTGTCACACAGC	2679
QY	2345	TTACGACTACCTGGTGTGACTGTATGAAGTATCTTCAATGAAGAAGGGCGTGTATTACGAA	2404
Db	2680	ATGAGCTACTTGGCCGACAGGTGTGACGTTCATCTATGCTATGAGTGGCCGACAGATCTCTGAG	2739
QY	2405	AGAGGCAACCCATGAGGAACCTGATGAATTTAAATGTGTACTATGCTACCATTTTAAATAC	2464
Db	2740	ATGAGGCTCTTACACGAGAGCTGTGGCTGAGACGGGCGCTTCGGTGAAGTTCTCTCGTAC	2799
QY	2465	CTGTCTCTGGGAAGACACCCTCAGTT---GAGTCAATTTCAAAAAAGAAACCAAGTGT	2521
Db	2800	TATGCCAGACACAGAGAGAGAGATGACAGAGAACGGGGTCAAGGGCGTCAAGGGGT	2859
QY	2522	TCACAGAAGAAAGTCACACAGCAAG-----GTCTTAATAACGATTCATAAAGAAAG	2573
Db	2860	CCAGGGAAGGAAGCAAAAGCAATGTGAAGATNGCATGTGCTGACAGGCACTGCAGGAAAG	2919
QY	2574	AAAAAGCAGTAAAGCCAGAGAAAGGCGAGCTGTGCAGCTG-----	2615
Db	2920	CAACTGCAAGACAGCTCAGACACTCTCTCTCTATAGTGGGGACATCACAGGCAACAC	2979
QY	2616	AAGAGAAAGGCGAGGGTTAGTCCCTCGTCACTATATGTGTCTATCATCAGGCTGCTG	2675
Db	2980	AACAGACACGACAGAACTGCAGAAAGCTGAGGCCACAGAAAGAGAGACCTGGAAGCTGATG	3039
QY	2676	GGGGC-----CCCTTGGCATCTCGTGAATTAATAGGCCCTTTTCAATGCGAATGTAGGC	2728
Db	3040	GAGGCTGCACAAAGCCGCAGACAGGCGCAGGTCAACCTTCCCTGTACTGGACTACATGAAG	3099
QY	2729	AGCACCGCCTTGACACACTGTGTGTGATTAGTTACTGTGATCAAGCAAGAGAACGGGAACCC	2788
Db	3100	GCCATGGAAGCTCTTCATCTCTCTCTCAGACATCTCTCTTCAATGTATACATATGTCTCC	3159
QY	2789	ACTGTGACT-----CGAGGAAACGAGACCTCGGTGATGTACACGATGAAGACATCTCT	2842
Db	3160	GGGTGTGCTTCCAACTATTTGGCTCAGCCCTCTGTGACTGATACCCCATCTCAACGGGACT	3219
QY	2843	CATATGCACTACTATGTCCAGACATCTACGGCCCTCTCATATGSCACTCATNGCTGATCTGA	2902
Db	3220	CAGAGACACACGAATCCGGCTGAGCGCTTATAGAGCCCTGSGCAATTTTCAAGGGATC	3279
QY	2903	GCCATTCGAG-----AGTTGTCTTTGTCAAGGGGACGCTGGAGCTTCTCCGGCTG	2956
Db	3280	GCCGTGTTGGCTACTCATTAGGCCGTGTCTCATGTGGGGGATCTTGGCTTCCCGCTGTCTG	3339
QY	2957	CATTGACAGACTTTTCGAAGGATCTCTTCAAGCCCTATGAAGTTTGTGACAGACCCCC	3016
Db	3340	CACGTGTGACTCTGTGCACAGCATCTTCGGCTCAACCATAGCTCTTTGTGACGGACCCCC	3399
QY	3017	ACAGGAGAGATTCTCAACAGGTTTTCACAAAGACATGATGAAGTGAAGTGAACGGGCTGGCG	3076
Db	3400	AATGGGAACCTGTGTGAACCGCTTCTTCAAGAGAGCTGTGACACATGTGGCTCTCATGATCCG	3459
QY	3077	TTTCAGAGCCGAGATGTTTATCTCCAGAAAGTATCTGTGCTTCTTCTGTGTGGGAATGAT	3136
Db	3460	GAGTCATCAATGATTTCAATGGGCTCCCTGTTCAACGTCAATGTGTGCTCATCTGTTATC	3519
QY	3137	GCAGAGAGTTCCTCCGCTGTCTTGTGGCAGTGTGGGCCCCCTTCTATCTCTTTTCAAGTC	3196
Db	3520	CTGTGTGGCCACGCCCATTCGCGCATCATCATCCCGCTTGGCCCTCATCTTCTTCTG	3579
QY	3197	CTGACACATTTGTCCAGAGGTCTCGATGTGGGAGCCTGAAGCGTGTGACAAATATACGACAG	3256
Db	3580	GTCCAGAGGTTTCTAGTGGCTTCTTCCGGCAGCTGAAGGGCTGTGAGTGTGACGACGCG	3639
QY	3257	TCACCTTTCCTCTCCACATTCACGTCCACATACAGAGGCTTGTCCACATCCACGCTTAC	3316
Db	3640	TCCCCGGTCTATTCCTCATTTTCAACAGAGACTTGTCTGGGGGTACAGCTCATGTGAGGCTTC	3699
QY	3317	AATAAAGGCGAGAGTTTCTGCACAGATACCAAGAGCTGTGTGATGACAACCAAGCTCT	3376

D	b		3700	GAGGAGCGAGAGCCCTTCATCCACCAAGTGAACCTTAAGATTGGAGACAGAACCGAAGGCC	3759
O	y	3377	TTTTTTTGTTTAGGTGGATGCGGTGGGTGCCTGTGCGGCTGGACTCATCAGCATC	3436	
D	b	3760	TATTACCCAGCATGCGGCCACAAAGGTGGCTGGCGTGGCTGTGAATGTGTGGCCAC	3819	
O	y	3437	GCCCCTCATCACACCACAGGGGCTGATGATGTTCTTATCCAGGGCAGATTCCCCACCC	3496	
D	b	3820	TGCATCGTTGTTTGGTGGCCGTGTTTGGGGTATGTCAGGCCACAGGCTCAGTGTCTGC	3879	
O	y	3497	TATGGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGCTGTCAGATTACGCTC	3556	
D	b	3880	TTGGTGGCCCTCTAGTGTCTTACTCATTTGACAGTCCACACCTACTTAACTGGCTGGTT	3939	
O	y	3557	AGACTGGCATGTGACAGACAAGCTCGATTCACCTCGTGGAGAGATCAATCACTACTT	3616	
D	b	3940	CGGATGTCATGTGAATGGAAACCAATCGTGGCGGTGGAAAGCTTAAGAAGATATTCA	3999	
O	y	3617	AAGACTGTCTCTTGAAGCACTGCCAGATTTAAGACAAGGTCCTCCCTGACTGG	3676	
D	b	4000	GAGACTGTGAAA - - - GGAGGGGCCCTCGGCAAAATCCAGAGACACGTCGCCAGACGTGG	4056	
O	y	3677	CCCCGAGGGAGAGGAGACTTGTGAAGACGACAGATAGAGTACCGAGAAACCTCCCT	3736	
D	b	4057	CCCCAGGTGGGCGAGTGGAAATTCGGAATCTGCTCTGCTGCTACCGAGAGACTGGAC	4116	
O	y	3737	CTCGTCTTAAAGAAAGTATCTTCACAGATCAAACCTTAAAGAGAAATTGGCATTTGGGG	3796	
D	b	4117	TTTCGTTCTCAGGCATCATATGTCCAGATCAATAGGGGGAGAAAAAGTGGCATGTGGGG	4176	
O	y	3797	CGGACAGGATCAGGAGTCTCGTGGCGGGAGTGGCCCTTCCTCCGCTGTGTGGATTTATCT	3856	
D	b	4177	CGGAGGGAGTGGGAAGTGTCTCCGTGACCCTGGGCTTATTTTCGGATTAACGACTGTGCC	4236	
O	y	3857	GGAGGCTGCATCAAGATTGATGGAGTGAAGATAAGTATTTGGCTTCCGACCTCCGGA	3916	
D	b	4237	GAGGAGAGATCATCATCATGATGGCATCAATCGCAAGATCGGCTGCACAGACTCTGCC	4296	
O	y	3917	AGCAAACTCTATCATCTCTCAAGAGCCGGTGTCTGTCACTGTGACTGTCAATTAAT	3976	
D	b	4297	TTCAAGATCACATCATCCCCCAGGAGCCCTGTTTGTTCGGTTCCTCCGATTAAC	4356	
O	y	3977	TTGAGCCCTTCAACCGTACCTGTGAAGACCGAATTGGGATGCCCTGGAGAGACAC	4036	
D	b	4357	CTGGACCATTTACCCAGCTACTGTGATGAAGAAGTGTGAGTCCCTGTGAGACTGGCCAC	4416	
O	y	4037	ATGAAAGATGTATGTCTACGTACTCTGAAACTTGAATCTGAAGTATGAGAGATGG	4096	
D	b	4417	CTGAAGAGACTTGTGTACAGCCCTTCTGTCAAGCTTAGACATGATATGTGAGAAAGCGGG	4476	
O	y	4097	GATGATCTTCAAGTGGGGGAGAGCGGACGTTGTGATATGCTAGAGGCCCTGTCCGCCAC	4156	
D	b	4477	GAGAACTCACTGTGCGGGCAGCGCCACGCTTGTGTGCTTACGCCCGGGCCTTCTAGAGAG	4536	
O	y	4157	TGTAAATTTGATTTTAAATGAAGCCACAGCTGCCATGTGACACAGAGACGATTATG	4216	
D	b	4537	ACGAAATTCCTTGTGTGTGATGAGCGCACGGCAGCGGACCTGTGAACCGAGACCTTC	4596	
O	y	4217	ATTCAAGAGACCATCGAGAGGCAATTGTGAGACTATACCATGTGACCATTTGCCCATGCG	4276	
D	b	4557	ATCCAGTCCACCATTCGGACACAGTTTCGAGGACTGACCGTCTACCATGTGCCACCGG	4656	
O	y	4277	CTGCACACGGTCTAGGCTTCGATAGAGATTATGTGTGTGGTCCACAGGCGACAGTGTGTG	4336	
D	b	4657	CTCAACACCATCATGAGACTCAACAAGGATGTGCTTGGAAACAAAGGAATTCACAGAG	4716	
O	y	4337	TTTGAACCCCATTCGCTCTTCTG 4360		
D	b	4717	TACGGCCCCCATTCGAGACTCTCTG 4740		

RESULT 10

Db 3340 CAGGAGGACCTGCTCAGACAGATCTCGGCTGACCATGAGCTCTTTGAGGGGACCC 3399
OY 3017 ACAGGAGATTTCTCAGAGGTTTTCACAAAGACATGATGAGTGAAGTGAAGTGGCGG 3076
Db 3400 AGTGGACCTGCTGACACCGCTTCTCAGAGGCTGGAACAGAGTGCATGATCCG 3459
OY 3077 TTCCAGGCGGAGATTTTATCCAGAGCTTATCCGCTGCTTCTGTTGGGAATGATC 3136
Db 3460 GAGGTCATCAAGATGTTGATGGGCTCCCTGTTCAACGATTTGCTCCATGCTTATC 3519
OY 3137 GCAGAGCTTCCCGTGGTCTTGTGSCAGAGGAGGCGGCTGTATGCTCTTTTCACTC 3196
Db 3520 CTGCTGGGACGAGCCATGCGGCTCATCATCCGCTTGGCTTACTTCTTC 3579
OY 3197 CTGACATTTCTCCAGGCTCTGATTTGGAGCTGAAGCTGTGACATATACAGCAG 3256
Db 3580 GTCCAGAGGTTCTACGTGGCTTCCGCGAGCTGAAGCGGCTGAGTGGTCAAGCGCG 3639
OY 3257 TCACCTTCTCTCCGATACGTCACGATACAGGAGCTTGCACCATCCAGCTTAC 3316
Db 3640 TCCCGGCTTATTCCTCATTTACAGAGACTTGTGGGGTACGCTTACGAGCTTTC 3699
OY 3317 AATAAGGCGAGAGTTCTGACAGATACAGAGAGCTGTGATGACACCAAGCTCT 3376
Db 3700 GAGGAGCGAGAGCGCTTATCCACAGAGTACCTGAAGTGGAGACAAACAGAGCGC 3759
OY 3377 TTTTCTTTTGTAGCTGTGCGATGGCTGTGCTGTGCGGTGAGCTTATCAGCATC 3436
Db 3760 TATTACCCACATCTGCGCCACAGAGGCTGCGCTGCGGCTGAGAGTGTGGGCAAC 3819
OY 3437 GCGCTCATCACACAGGAGGCTGATGATGTTCTATGACAGGAGCAATTCGCCACCC 3496
Db 3820 TGCACTGCTTCTGTTGCTGCGCTGTTGGCTGATCTCCAGGACAGCTTACGCTGCG 3879
OY 3497 TATCGGGCTTCGCGCATCTTATGCTGTGCTGATTAACGGGCTGTGCTTACATTCGCTC 3556
Db 3880 TTGGTGGGCTCTCAGTGTCTTACTCATTTGAGGTCACACAGTACTTAACTGGCTGTT 3939
OY 3557 AGACTGGCATCTGAGACAGAAAGCTGATTCACCTGGGTGAGAGAGATCACTACATT 3616
Db 3940 CGGATGTCATCTGAATGGAACCAACATCTGCGCTGAGAGAGCTCAAGAGATTTCA 3999
OY 3617 AAGACTGTCTTGAAGACCTGCCAGATTAAGAAAGAGCTCCCTCCCTGACCTGG 3676
Db 4000 GAGACTGAGAA---GGAGGCGCCCTGCGAAATTCAGGAGACAGCTGCGCAGACAGCTGG 4056
OY 3677 CCCCAGAGAGGAGAGGAGCTTTGAGAACGACAGAGATGAGTACCGAGAAACCTCCCT 3736
Db 4057 CCCCAGAGTGGGCGAGTGGATTCGGGAATTAAGCTGCGCTTACCGAGAGAGCTGGAC 4116
OY 3737 CTGCTCTTAAGAAAGATCTTACGATCAACCTTAAGAAAGATTTGGCATTGGGG 3796
Db 4117 TTCTGTTCTCAGGACATCAATGATGAGTCAATGGGAGAAAGATCGCATGCTGGG 4176
OY 3797 CGGACAGGATAGGGAAGTCTGCTGGGAGATGGCCCTTCCTCGTGGTGAATATCT 3856
Db 4177 CGGACGAGAGTGGGAAGTCTGCTGAGCCCTGAGCTTATTTGGAATCAACAGAGTGGC 4236
OY 3857 GAGGCTGATCAAGATGATGAGTGAAGATGATGATTTGGCTTGGCAGCTCCGA 3916
Db 4237 GAAGGAGAGATCATCATGATGATGATCAACATGCGCAAGATGGCTGCAAGAGCTCCG 4256
OY 3917 AGCAACTCTCTATCATTTCTCAAGAGCGGCTGTTCAGTGGCAGCTGATCAAT 3976
Db 4297 TTCAAGATTCACATATCCCGCAGAGACCTGTTTGTGTTGGGTCCCTCGAATGAC 4356
OY 3977 TTGAGACCTTTCACACGATGATGAGAGACAGATTTGGGATGGCTGGAGAGACAC 4036
Db 4357 CTGAGCCATTCAGCGAGTCTGATGAGAAAGTGGAGCTCCCTGGAGCTGGCCAC 4416
OY 4037 ATGAAGATGATTTGCTGCTACCTCTGAAACTGATGAAGTGAATGGG 4096

Db 4417 CTGAAGGACTTCTGTCACCCCTTCTGACAACTAGAACCATGAATGTGACAGAGCGG 4476
OY 4097 GATACTTCTCAGTGGGGAACGCGAGCTCTTGTGATAGTAGAGCCCTGCTCCGAC 4156
Db 4477 GAGAACCTCAGTGTGGGAGCGGAGCGCTGTGTGCTAGAGCCCGGCTGCTGAGAA 4536
OY 4157 TGTAAAGTTCGATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 4216
Db 4537 ACGAAGATCTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4596
OY 4217 ATTCAAGAGACCATCGGAAGACATTTGACAGCTGATACATGCTGACCATGGCCATGC 4276
Db 4597 ATCCAGTCCAGCATCCGAGACAGTTCAGAGACTGCTGCTTACCATGCGCCACCG 4656
OY 4277 CTGACAGGTTCTAGGCTCCGATAGATTTATGATGATGATGATGATGATGATGATGAT 4336
Db 4657 CTCAACACCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4716
OY 4337 TTGACACCCCATGCGCTCTCTG 4360
Db 4717 TACGGCGCCCATGCGACCTCTG 4740

RESULT 11
US-08-462-109A-1
Sequence 1, Application US/08462109A
Patent No. 5882875
GENERAL INFORMATION:
APPLICANT: Cole, Susan P. C.
APPLICANT: Dealey, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,109A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-Oct-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-Oct-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deconlt, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: P01-002CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

OY	2405	AAAGCACCCTGAGGAAACGATGAATTAATTAAATGAGACTAATGCTACCAATTTTATATAC	2466
Db	2740	ATGGGCTCTTCAACAGAGAGCTGCTGGCTCGAGAGGGGCGCTTGCTAGTTTCTGGCTAC	2799
OY	2465	CTGTTGCGGAGAGACACCGCCAGTT---GAGATCAATTTCAAAAAGGAAACAGTGT	2522
Db	2800	TATGCCACACAGAGCAGAGACAGAGATGCGAGAGAAACGGGGTCAAGGGCTCACGGCTCACGGGT	2855
OY	2522	TCACAGAAGATCAACAAGACAAAG-----GTCCTAAACAGGATCAATTAAGAG	2573
Db	2860	CCAGGGAAGCAAGCAAAAGTAATGGAATGAGCATGCTGTTGACGGACAGTGCAGGAG	2919
OY	2574	AAAAAGCATTAACCCAGAGAAAGGACGCTTGTGACGTG-----	2615
Db	2920	CAACTGCAGACAGAGCTCACACACCTCCTCCTTAAGGGGACATCAGACGACACC	2979
OY	2616	AAGAGAAAGGCGAGGGTTCAGTGCCGCTGGCTAGTATATGTCATATCCAGGGCTGTG	2675
Db	2980	AMCAGCACCGCAGACATGCGAAAAAGCTGAGGCCAABAAGAGAGACCTCGAAGCTGATG	3039
OY	2676	GGGG-----CCCTGGCATTCCTGGTTATTAATGAGCCCTTTCAATGCTGAATTAAG	2728
Db	3040	GAGGCTGCAGAGGCGCAGACAGGCGAGGTCACACTTTCGCTGACGGGACTACATTAAG	3099
OY	2729	AGCACCGCCTTCAGCACCTGCTGCTGTTAGTTACTGATCAACAGAGAGCGGGAACAC	2788
Db	3100	GCCATCGAGACTTTTCAATCTCCTTCACAGATCTTCTTTTCAATGTAACCATGTGTC	3159
OY	2789	ACTGTGACT-----CGAGGAAACGAGACCTCGGTGAGAGACGATGAAGGACAACT	2842
Db	3160	GGCGTGGCTTCCAACTTTTGGCTCAGCTCTGTGACTGATGACCCCACTGTCAACGGGACT	3219
OY	2843	CATATGCAGTACTATGCCACATCTACGCCCTTCATGAGCATGCTGATCTCTGAA	2902
Db	3220	CAGAGACACACGAAAGTCGCGGTGAGGTCATGAGACCCCTGGGACTTTTCAACAGGATC	3279
OY	2903	GCATTTGGAGS-----AGTTGTCTTTGTTCAGAGGCGAGCTCGAGCTTCTCCGGCTG	2956
Db	3280	GCCGTGTTTGGCTACTCAATGAGGCCGTGCTCATCGGGGGGATCTTGGCTTCCCGCTGTC	3339
OY	2957	CATGACGAGCTTTTCCGAGAGATCTTCGAAAGCCCATGATCTTTTGTGACACGACCCC	3016
Db	3340	CACGTGGACCTGCTGCGACACATCTTGGCTACCCATAGCTTTCTTTGAGCGGACCCCC	3399
OY	3017	ACAGGAGAGATTCTCAACAGGTTTCCAAAGACATGATGAAGTTGACGTGGCGCTGCCG	3076
Db	3400	AGTGGAAACCTGGTGAACCGCTTCTCCAAAGAGCTGTGAACAGTGAATCCATGATCCG	3459
OY	3077	TTCCAGGCCGAGATGTTCAATCCGAAACGTTATCTGTGTTCTTCTGTGTGGGAATGATC	3136
Db	3460	GAGGTCAATCAAGATGTTCAATGAGGCTCCCTGTTCAACGTATGTGGCTGCATCGTATATC	3519
OY	3137	GCAGAGAGCTTCCCGGTGGTTCCTTTGGGACAGGGGGCCCTGTATCTCTTTCACT	3186
Db	3520	CTGTGGCCACGCCCATATCCGCCGCAATCATTCGCCCTTGGCTATCTACTTCTTC	3579
OY	3197	CTGCACATTGCTTCCAGAGGTCCTGATTGCGGAGCTGAACGCTGTGGAATAATCAACGAG	3256
Db	3580	GTCACAGAGGTTTACAGGGCTTCTCCCGGACAGCTGAACGGCTGTGAATCGGTACGCCG	3639
OY	3257	TCACCTTCTCTTCCACATCAGTCCAGCATACAGGGCTTTGCCACATCCAGCCCTAC	3316
Db	3640	TCGCCGGGTATTTTCTTCTTCAACGAGACCTGTGGGGGTGAGGTATTTCTGAGACCTTC	3699
OY	3317	AATTAAGAGGAGAGATTTCGACAGATATCCAGAGGCTGCTGGATGACAAACCAAGCTCT	3376
Db	3700	GAGAGCAGAGAGCGCTTCAATCCACAGAGTGAATCTGAAGTGGAGCAACACAGAGGCC	3759
OY	3377	TTTTTTTGTATACGTGTGCGATGATCGGCTGGCTGCTGTCGCGCTGAGCTCATCAGATC	3436
Db	3760	TATTATCCCAACAGATCGTGGCCCAACAGTGGCTGCGCGTGTGAGATGTGTGTGGCAAC	3819
OY	3437	GCCCTCATCACACACGGGGCTGATGATGCTTTTATGCACGGGACAGATTTCCCAACC	3496

Db	3820	TGCATCGTTCTGTTTGGCTGGCCCTGTTTGGCGGTATATCTCAGGACAGACCTCAGTCTGGC	3875
OY	3497	TATGGGGGCTTCGGCAGTCATCTCTTATGCTGTGCAGTTAAAGCGGGCTGTTCAGTTAAGGTC	3556
Db	3880	TTGGTGGGCTCTCTAGTGTCTTACTACTTTCCAGGTACACCACTACTTGAATGCGCTGGTT	3933
OY	3557	AGACTGGCATCTGAGACAGAAGGCTCGATTCACCTCGGTGGAGAGATCAATCACTACATT	3618
Db	3940	CGGATGTCTATCTGAATATGAAACCAACATCATGTGGCGGTGGAGAGCGTCAAGAGATATTC	3999
OY	3617	AAGACTCTGTCTTTGGAAGCACTGCCAGATTAAACACAAAGGCTCCCTCCCTCACTGG	3678
Db	4000	GAGACTGTGAA - - -GGAGGGCGCCCTGGCAATTCAGAGAACACATCTCCGCTCAGCAGCTGG	4056
OY	3677	CCCCAGGGAGGAGAGGAGGACCTTTGGAAGACGAGATAGAGTACCGAGAAACCTCCCT	3738
Db	4057	CCCCAGGTGGGCGCAGGGAATTCGGAACTACTGCTCGCTGGCTACCGAAGAGACTGGAC	4118
OY	3737	CTCGTCTTAAAGAAAGTATCTCTTCAGATCAAACTAAAGAGAAATTTGGCATTTGGGG	3796
Db	4117	TTTCGTTTCAAGGCATCATCATATGTCCAGATCAATGGGGGAGAAAGTGGCATTCGTGGGG	4176
OY	3797	CGGACAGGATCAGGGAAGTCCCTGCTGGGGAGTGGCCCTTCCGTCGTGTGAGTTATCT	3856
Db	4177	CGGACGGGAGCTGGGAAGTGTCCCTCGACCTCGGCTTGGCTTTTCGGATCAACAGTCTGCC	4236
OY	3857	GGAGGCTGCATCAAGATTGATGTGAGTGAAGATAGATATTGGCTTCCGACCTCCGA	3916
Db	4237	GAGGAGAGATCATCATCATATGAGATCAATCATGATGCCAATATGGCTTCAGCACTCCGC	4296
OY	3917	AGCAAACTCTCTATCATTTCTCTCAAGAGCCGGTCTCTTGAAGGCACTGTTCAGATCAAT	3978
Db	4297	TTCAAAATACACATCATATCCCCAGGAACCGTGTTTTGTGGGTTTCCCTCCGATTAAC	4356
OY	3977	TTGGAACCCCTTCAACAGTACACTGAAGACAGATTTGSGAATGCCCTGGAGAGACAC	4036
Db	4357	CTGGACCCATTCACGCCAGTACTCGGATGAAGATCTGGACCTCCCTGGAGCTGGCCAC	4416
OY	4037	ATGAAAGATGTATTTGCTGACGTACGCTGAAACCTTGATCTGAAGTATATGAGAAATGGG	4096
Db	4417	CTGAAAGACTTTCGTGTACGCCCTTCTCGACACGTAGACCATGAAATGTGCMAAGGCGGG	4476
OY	4097	GATAACTTCTCAGTGGGGGGAAGCGCAGCTTTGTGATAGCTAAGACCCCTGCTCCGCCAC	4156
Db	4477	GAGAACTCAGTGTGCGGGACGGCCAGCTTGTGTGCTTACGCCGGGCCCTGTGTAGGAAG	4536
OY	4157	TGTAAATTTCTGATTTTAAATGAAGACACAGCTGACGTCATGAGCAGACAGACTTATTG	4216
Db	4537	ACGAAAGATCTTGTGTGTGAATGAGGCGCACGGCAGCCGTGGACTGAAACGAGACACTC	4596
OY	4217	ATTCAGAGAGCAATCCGAGAAAGATTTGCAAGCTGTACCATCTGACCATTTGCCATGCG	4276
Db	4597	ATTCAGTCCACATTCGCGGACACAGTTGTGAGAGATGACCTGCTCTCAATCCGCCACGG	4656
OY	4277	CTGCACACAGGTTTACGCTCCGATAGAGATTATGTCCTGGCCAGGACAGGTGGTGGAG	4336
Db	4657	CTCAACACATCATGAGCTACACAAAGGATGTGTGTTGACAAAGGAAATCCAGAG	4716
OY	4337	TTTGACACCCCATCGTCTCTTGG 4360	
Db	4717	TACGGCGCCCATCGACCTCTGG 4740	

RESULT 13

US-08-463-179A-1

; Sequence 1, Application US/08463179A

; Patent No. 6001563

; GENERAL INFORMATION:

; APPLICANT: Cole, Susan P.C.

; APPLICANT: Deesley, Roger G.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS

; NUMBER OF SEQUENCES: 6

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RESULT 13
US-08-463-179A-1
; Sequence 1, Application US/08463179A
; Patent No. 6001563
;
; GENERAL INFORMATION:
;
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Debley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
; NUMBER OF SEQUENCES: 6

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```

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,179A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: POI-002CP8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..4788
US-08-463-179A-1

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Query Match          10.4%; Score 506.4; DB 3; Length 5011;
Best Local Similarity 52.4%; Pred. No. 1.3e-121;
Matches 1364; Conservative 0; Mismatches 1181; Indels 59; Gaps 9;

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QY 1811 CACATCCACCTGGGCACTGCTTACAGAGACACTGCACAGCATCGATCGAGATC 1870
DB 2142 CACATTCACCTGGGCA--GGAGGACCCCTCCACACTGAATGCACTTCTCCATC 2199
QY 1871 CAGAGAGGTAACCTGGTTCATCTGCGGCACTGTGGAAAGTGAACCTCTCAT 1930
DB 2200 CCGAAGGTCCTTGTGGGCGGTGGTGGCCAGGTGGCGGAAAGTGTCCCTGCTC 2259
QY 1931 TCAGCCATTTTAAAGCCAGATGACGCTTCTAGAGGCGAGCATTTGAACAGTGAACCTTC 1990
DB 2260 TCAGCCCTCTTGGCTGATGAGACAAAGTGAAGGCGACGCTATTCAGAGGCTCCGTG 2319
QY 1991 GCTTATGTGGCCAGCAGGCGCTGATCTCAATGCTACTCTGAGAGCAACATCTGTTT 2050
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QY 2051 GGAAGGAATATGATGAAGAAATACACTCTGTGCTGAACAGCTGCTCCTGAGGCT 2110
DB 2380 GGAATGTCAGTGAAGCAACATATTTACAGGTCCGTGATACAGGCTGTGCTCCCTCCA 2439
QY 2111 GACCTGGCATTCTCCAGCAGCAGACCTGACGAGATGAGAGGAGCAGAGCAACCTG 2170
DB 2440 GACCTGGAATCTCTGCCAAGTGGGATCGAGCAGAGATGGCGAAGAGGCGTGAACCTG 2499

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QY 2171 AGCGTGGGCGAGCGCCAGAGGATCAGCTTGGCCGGGCGCTTATATGACAGAGCATC 2230
DB 2500 TCTGGGGACACAGAGAGCGCGTGAACCTGGCCGGCGCTTACTCCACCTGACAT 2559
QY 2231 TACATCTGGAGACCCCTCAGTGCCTTATATGCCATGTGGGCAACCATCTTCAAT 2290
DB 2560 TACCTCTTGATGATGCCCTTCAGAGTGAATGCCCATGTGGGAAACATCTTTGAA 2619
QY 2291 AGTGCAT-----CGGAACATCTCAAGTCCAAAGACAGTTCTGTTGTAACCAACG 2344
DB 2620 AATGATTTGGCCCAAGGGATGCTGAAGAAACAGACGCGATCTTGATCAGCAGAC 2679
QY 2345 TTACAGTACCTGTTGACTGATGATGAAGATCTTCAATGAAGAGGCGCTTATACGAA 2404
DB 2680 ATGACCTACTTCCCGAGGTGACGTCATCATGTGATAGTGGCGCAAGATCTGAG 2739
QY 2405 AGAGCACCACATGAGGAATGTATTAATGTGATATGCTTACCATTTTATTAAC 2464
DB 2740 ATGGGCTCTTACCAGAGAGTGTGCTGAGAGCGCGCTTGCCTGACTTCTGCTTACC 2799
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DB 2800 TATGCCACACAGAGCAGAGAGGATGACAGAGAGAAACGGGGTTCAGCGGT 2859
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DB 3100 GGCATGCGACCTTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3159
QY 2789 ACTGTGACT-----CGAGGACAGAGACCTCGGTGATGACAGATGAAGACAAATCT 2842
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QY 2843 CATATGACGATCTATGCGAGCATCTACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2902
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Db 3580 GTCCAGAGGTTCTACGGGCTTCTCCCGGACCTGGAAGGCGCTCGGTCGACGCGC 3639
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Db 3820 TGCATGCTCTGTTTCTGCTGCGCTGTTTGGCGTATCTCAGGACAGCCCTCAGTGTGC 3879
QY 3497 TATCGGGTCTCGCATCTCTTATGCTGATGCTTAACGGGGCTGTTCCAGTTACGGTC 3556
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Db 4000 GAACCTGAGAA--GGAGGGGCGCTGGCAATCAGAGAGACAGCTCGCCACAGATGG 4056
QY 3677 CCCCAGAGGAGAGAGTGAACCTTGGAGAACGAGATGAGTACCGAGAAACCTCCCT 3736
Db 4057 CCCCAGTGGCGCGAGTGGAAATTCGGAACTACTGCTGCGCTACCGAGAGAGCTGGAC 4116
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Db 4117 TTGCTTCTCAGGACATCATGTCAGATCAATGGGGGAGAAAGGTCGATCTGGGG 4176
QY 3797 CGGACGAGATCAGGAGAGTCTCGGCGGGAGTGGCCCTCTCCCTCGGTCGAGTATCT 3856
Db 4177 CGGACGAGAGTGGAGAGTCTCGGCGGGAGTGGCCCTTATTTTGGATCAACAGTGTGC 4236
QY 3857 GGAGGCTGCAATCAAGATTGATGAGATGAGATGATGATGAGTGGCCCTCGGACCTCGA 3916
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QY 3917 AGCAAACTCTATTCATCTCTCAAGAGCGGCTGCTGATGATGATGATGATGATGAT 3976
Db 4297 TTCAAGATCAGCATATCCCGGAGAGCGGCTGTTTGGTTCGCGGTTCCCGAATGAC 4356
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Db 4357 CTGGACCCCATTCAGCAGTATCGATGAAAGTGTGAGCGTCCCTGGAGCTGGGCCAC 4416
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Db 4417 CTGAGAGACTTGTGTGAGCGCTTCTGACAGACTAGACCATGATGATGAGAGCGGG 4476
QY 4097 GATTACTTCTCAGTGGGGGAGAGCGGCTTGTGATAGACTAGAGCCCTGCTCGGCAC 4156
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QY 4157 TGTAAATCTGATTTTGAATGAGGACAGCTGCCATGACACAGAGACATTTTG 4216
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Db 4657 CTCACACCATCATGAGCTACACAGAGGTGATGCTTTGGACAAAGGAAATCCAGAG 4716
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RESULT 14
US-08-461-384B-1
; Sequence 1, Application US/08461384B
; Patent No. 6025473
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,384B
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: 01547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-461-384B-1

Query Match 10.4%; Score 506.4; DB 3; Length 5011;
Best Local Similarity 52.4%; Pred. No. 1,3e-121;
Matches 1364; Conservative 0; Mismatches 1181; Indels 59; Gaps 9;
QY 1811 CACATCACCTGGGCGCATGCTTACAGAGACACTGCACAGCATGATCTGGAGATC 1870
Db 2142 CACATTCACCTGGGCGCA--GGAGGAGACCTCCACACTGAATGACATCACTTCCATC 2199
QY 1871 CAAGAGGATTAATGCTGTGAATCTGGGAGTGTGGGAAGTGGAAAACTCTCAT 1930
Db 2200 CCGGAAGTCTTGTGGGCGGTGTGGGCGAGGTGGCGGAAAGTTTCCCTGCTC 2259
QY 1931 TCAGCATTTAGGCGCATGAGCTTCTAGAGGCGAGCATGCAATCAGTGAACCTTC 1990

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Db 2380 GGATGTCACTGAGAGAAACATATTAACAGTCCGTGATACAGGCTGTCCTCTCCA 2439
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Db 2440 GACCTGGAATCTCGCCAGTGGGATGGAGACAGATTTGGGAGAGGCGCTGAACG 2499
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Db 2620 AATGTATTTGGCCCCAAGGGATGCTGAAGAAACAGCGGATCTTGTGTCAGCAGC 2679
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Db 3100 GCCATCGGACTCTTCATCTCTCTCAGATCTCTCTTTCATGTGTAACATGTGTCC 3159
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Qy 3077 TTCAGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3136
Db 3460 GAGGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3519
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Db 4417 CTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4476

OY	4097	GATATCTTCACAGGGGGGAAAGGACAGCTTGTGATAGTAAAGACCTGCTCGGCAC	4156
Db	4477	GAGAACTCAGTGTGCGGGACAGCCACAGCTTGTGTGCTTAGCCCGGGCCTTGCTGAGAG	4536
OY	4157	TGTAAATTTTGAATTTTAAATGATGAAGCCACAGCTGCCATGAGACACAGACAGATTATG	4216
Db	4537	ACGAAAGATCCTTGTGTGTGATGAGGCCACAGCGACCGTGTGACTGGAAGCGAGACCTC	4596
OY	4217	ATTCAAGAGACCAATCCGAGAGAGCATTTGACAGCTGTACATCTTACCATTTGCCATCGC	4276
Db	4597	ATCCAGTCCACACATCCGAGACACAGTTCTGAGAGACTGTACCGCTCTTACCATGCGCCACCG	4656
OY	4277	CTGCAACAGGTTCTAGAGCTCCGATATGAGATTATGTGTGTGGCCAGACAGAGTGTGTGG	4336
Db	4657	CTCAACACACCTCATGAGACATCAACAGGAGTGATCTTTTGAGCAAAAGAGAAATCCAGAG	4716
OY	4337	TTTGACACCCCATCGAGCTCTCG	4360
Db	4717	TACGGGCCCCATCGAGACTCTCG	4740

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RESULT 15
US-08-407-207A-1
Sequence 1, Application US/08407207A
Patent No. 6063621
GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P. C.
TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
City: Kingston
STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,207A
FILING DATE: 20-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01512
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ. ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..4788
US-08-407-207A-1

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Query Match	Similarity	10.4%	Score	506.4	DB	3	Length	5011
Best Local	Similarity	52.4%	Pred	No.	1.3e-121			
Matches	1364	Conservative	0	Mismatches	1181	Indels	59	Gaps
QY	1811	CACATCCACCTGGGGCCACCTGCGCTTACAGAGACACTGACACGATCGATCTGGAGATC	1870					
DB	2142	CACATTCACCTGGGGCCA - GGAGCCACCCCTCCACACTGAATGAGCATCCCTTCACATC	2199					
QY	1871	CAGAAGGCTAACTGGTTGGAAATCTGCGGCATGTGGGAAGTGGAAAACTCTCATTT	1930					
DB	2200	CCCGAAGGTGCTTTGGTGTGGCCGCTGGTGGCCAGGTGGGCTGGGAAAGTTGTCCCTGCTC	2259					
QY	1931	TCAGCCATTTTTGGCCAGATGACGCTTCTAGAGGCGAGCATGTGCATAGTGAACCTTC	1990					
DB	2260	TCAGCCCTCTTGGCTGATGATGACAAAGTGGAGGGGACGTGGCTATCATAGGGGCTCCGTTG	2319					
QY	1991	GCTTATGTGCCCCACAGACGCTGTGATCCTCAATGCTACTCTGAGAGACAACTCTGTTT	2050					
DB	2320	GCCCTATGTGCCACACACAGCCCTGTGATTCAGAAATGATTTCTTCCCGAAGAAACATCTTTT	2379					
QY	2051	GGGAAGGAATATGATGAAGAAATACAACTGTGCTGAACAGCTGGCTGAGGGCT	2110					
DB	2380	GGATGTCACTGTGGAGGAACCATATTACAGCTCCGTGATACAGGCTGTGCTCTCCCA	2439					
QY	2111	GACCTGGCCATTCTTCCAGACGACGACCTGACGGAATTTGAGAGCGAGGACCAACTG	2170					
DB	2440	GACCTGGAAATCTCCACAGTGGGGATGAGACAGATATGGCGAAGAGGCGCTGAACCTG	2499					
QY	2171	AGCGGTGGGCAAGCCGACAGAGATCAAGCCTTGGCCGGGCTTGTATATGTACAGAGACATC	2230					
DB	2500	TCTGGGGGACAAACACACGCGCTGAGCCTTGGCCGGGCTGTACTCCAAACCTGACATT	2559					
QY	2231	TACATCTGTGAGAGACGACCCCTCAGTGCCTTATGATGGCCATGTGGGCAACACATCTTCAT	2290					
DB	2560	TACCTCTTGATGATGCCCTCTCAGACAGTGGATGCCATGTGGGAAACACATCTTTGAA	2619					
QY	2291	AGTGTAT - - - - - CCGAAGACATCTCAAGTCCAAGACAGTTCTGTTTTCACCAACAG	2344					
DB	2620	AATGTGATTTGGCCCCCMAAGGGGATGCTGGAAGAAACAGCGGATCTTGTGTCACGCACAGC	2679					
QY	2345	TTACAGTACCTGGTTGACGTGTGATGAAGATCTTCATGAAGAAAGAGGGCTGTATTACGAA	2404					
DB	2680	ATGAGCTACTTGGCCGAGAGTGACCTCATCATCGTATGAGTGGCGGCAAGATCTCTGAG	2739					
QY	2405	AGAGGACCCCATGAGGAACGTGATGAATTTAAATGCTGACTATGTCATACCATTTTATATAC	2464					
DB	2740	ATGGGCTCTTACACAGAGACTGTGCTCGAAGCGGGCTTCGCGATTCCTGCGGTAC	2799					
QY	2465	CTGTGCTGGAGAGACACCCCACT - - - GAGATCAATTCAAAAAGGAACCAAGTGT	2521					
DB	2800	TATGCCACACAGACAGACAGAGAGGATGCAGAGGAAACGGGGTTCACGGGCTCAGCGT	2859					
QY	2522	TCACAGGAAGTGTCAAGACAAAG - - - - - GATCAAAAAACAGATCAATTAAGAAAG	2573					
DB	2860	CCAGGGAAGGAAGCAACAACTGAGAAATGAGCAATGCGATGCTGTGACGACAGTGCAGGAAG	2919					
QY	2574	AAAAAGCAGTAAGGCCAGAGGAAGGAGCTGTGACAGCTG - - - - -	2615					
DB	2920	CAACTGTAGAGACACTGACAGAGCTCTCTCTCTATGTGGGAGATCATGACGAGCAACC	2979					
QY	2616	AAGGAAAGGCGCAGGGTTCACTGCCCTGTGTCATGTATGTGTCTTACATCCAGGCTGCTG	2675					
DB	2980	AACAGCACCGCAGAACTGCACAAAGCTGAGGCCAACAAAGAGAGACCTGGAGAGCTGATG	3039					
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 09:17:10 ; Search time 5627.18 Seconds
(without alignments)
18635.330 Million cell updates/sec

Title: US-09-528-031-1

Perfect score: 4847
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 1081749327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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4	4792.6	98.9	5838	61	US-60-226-176-205	Sequence 205, Appl1
5	4792.6	98.9	5838	62	US-60-233-468-205	Sequence 205, Appl1
6	4792.6	98.9	5838	70	US-60-313-371-205	Sequence 205, Appl1
7	4775.4	98.5	4781	12	US-08-843-459-1	Sequence 1, Appl1
8	4304.4	88.8	4314	61	US-60-226-176-206	Sequence 206, Appl1
9	4304.4	88.8	4314	62	US-60-233-468-206	Sequence 206, Appl1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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36 725.4 15.0 4638 35 US-09-934-421A-1 Sequence 1, Appl1
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38 703.8 14.5 4753 17 US-09-396-885-4872 Sequence 4872, Ap
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40 703.8 14.5 4753 17 US-09-428-151A-9221 Sequence 9221, Ap
41 684.6 14.1 900 25 US-09-644-870-7500 Sequence 7500, Ap
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43 684.6 14.1 900 25 US-09-652-915-8826 Sequence 8826, Ap
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45 651.2 13.4 4480 25 US-09-644-870-9947 Sequence 9947, Ap

ALIGNMENTS

RESULT 1

US-09-528-031-1

Sequence 1, Application US/09528031

GENERAL INFORMATION:

APPLICANT: SHYJAN, Andrew

TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED

POLYPEPTIDE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/528, 031

FILING DATE: 17-Mar-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth A. Hanley

REGISTRATION NUMBER: 33,505

REFERENCE/DOCKET NUMBER: MNI-056CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4847 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 116..4426

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-528-031-1

Query Match

Best Local Similarity 100.0%; Score 4847; DB 19; Length 4847;

Matches 4847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT    4
US-60-226-176-205
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; GENERAL INFORMATION:
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Malsen, Gareth
; APPLICANT: Townley, David
; APPLICANT: Morris, MacDonald
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
; FILE REFERENCE: GX-0013-1-P
; CURRENT APPLICATION NUMBER: US/60/226,176
; NUMBER OF SEQ ID NOS: 2447
; SOFTWARE: PERL Program
; SEQ ID NO 205
; LENGTH: 5838
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GB:AFL04942
US-60-226-176-205

Query Match          98.9%, Score 4792.6; DB 61; Length 5838;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4809; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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RESULT 5
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 ; GENERAL INFORMATION:
 ; APPLICANT: Ring, HuiJun Z.

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? APPLICANT: Malsen, Careth
? APPLICANT: Townley, David
? APPLICANT: Morris, MacDonald
? APPLICANT: Valdes, Ana
? TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated with ADME Genes
? FILE REFERENCE: GX-0013-2 P
? CURRENT APPLICATION NUMBER: US/60/233,468
? CURRENT FILING DATE: 2000-09-18
? NUMBER OF SEQ ID NOS: 2488
? SOFTWARE: PERL Program
? SEQ ID NO 205
? LENGTH: 5838
? TYPE: DNA
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D	1931	ctctctatttcagcatctttagccagaatgcactctctaaaggagcagcatctgcaatcag	1990
Q	1981	TGGAAACCTTGCTTATGTGTGGCCAGACAGCCCTGGATTCCTCAATGCTATCTCGAGAGCAA	2040
D	1991	tggaacctctgcctctatgtgtgcccagaagcccgatccccaatgcactccgaaagaaaa	2050
Q	2041	CATCTGTTTGGGAGAAATATGATGAAAGAAATACAATCTGTGCTGAACACACTGCTG	2100
D	2051	catctcgttttggaagaaatataatgataagaagaatacaactctgtgctggaacagctgctg	2110
Q	2101	CTGTAGGCGCTGACCTGCGCATTTCTTCCAGCGACCACTGACGGAGATTTGAGAGCGAG	2160
D	2111	ccctgagccctgcacctgcgcacatctctccacagcagcactgcagagatctgaaagcgaag	2170
Q	2161	AGCCAACTGAGGGGGGAGCGAGCGCCAGAGATGTCAGCCTTGCCGGGCGCTGTATTAGGA	2220
D	2171	agccaaacctgagcgtgtgaggcagcgcagagatcagcctctgcgcgggcccctgtatagga	2230
Q	2221	CAGGAGCATCTACATCCTGTGAGACGCCCTCTGATGCTTATGATGCCATGTGGCAACA	2280
D	2231	caggagatctatactctctgagcgaacccctcagtgacctagatgcccctgtgtggcaaca	2290
Q	2281	CATCTTCAATATGTCCTATCCGGAACATCTCAAGTCCAAAGACAGTTCTGTTGTATCCCA	2340
D	2291	catcttcaatagtgcatctccgaaacatctcaagatccaaagacagcttcgtctgtaccca	2350
Q	2341	CCAGTTACATCTACTCTGTTGACGTCGATGAATGAATGATTCCTTCAAGAAAGGGCTGTATTAC	2400
D	2351	ccagttacatcagtaacctgtgtgcacgtgtgaatgaaatgcatcttcaagaagaggcgctatcac	2410
Q	2401	GGAAGAGGACCCCAAGAGGAACCTGATGAATTTAATAGTGTGACATCTGTGTACATTTTAA	2460
D	2411	ggaaagagggaacccatcagtagaaactgaatcttaaaatggtagacatgtctaccatctttaa	2470
Q	2461	TAACTGTGTCGTGGAGAGACACCGCCAGTTGAGATCAATTTCAAAAAAGAAACCACTGG	2520
D	2471	taacctgtctgtgagagagacacgcgcagcttgagatccaatcaaaaagaaacacagctgg	2530
Q	2521	TTCAACAGAAACATCTACAGACAGCAAGGCTCTTAAACAGAGTCAATAAAGAGAAAAAC	2580
D	2531	ttcaacagaagaatctacaagaacaaggtctcttaaaacagatctcagtaaaagaagaaaaagc	2590
Q	2581	AGTAAAGCCAGAGAGAGGCGAGCTTCTGACGTGGAGAGAAAGGCGGGTTCAAGTCC	2640
D	2591	agtaaaagccagaggaagggcagcgtctgtcagctctgaaagaagaaagggcagggcttcagtgcc	2650
Q	2641	CTGGTCAGTATATGTGTCTACATCCAGGCTCTGGGGGCCCTTGGCATTCCTGATTAT	2700
D	2651	ctgtgcagataatgtygtcttaacatccaggtcgtctggggccctctggatctcctgatat	2710
Q	2701	TATGGCCCTTTTATATCTGATATGTAGAGACACCGCCTTTCAGACACTGTGTGTAATTA	2760
D	2711	tatggtcccttcttatctcttaattgtagcagcaccgcctctcagcacttgtygtctgagta	2770
Q	2761	CTGTGATCAAGCAAGAAAGGGGGAACCAACCTGTGACTGAGAGAAAGAGACCTCGGTGAG	2820
D	2771	ctgtgatacaagcaaggaagcgggaaacecacctgtgcactcgaaaggaaacgagacatctgtgag	2830
Q	2821	TGACAGCATGAAGGACAAATCTCATATATGCAATGCAATGATCCAGACATCTACGCCCTCTCAT	2880
D	2831	tgacagcatgaaggaacaatcccatatgagtactatgacagatctacgacccctccat	2890
Q	2881	GGCAGTCATGCTATATCTCTAAAGCAATTCGAGAGATTTGTCTTTTCAAGGGCACGCTGCG	2940
D	2891	ggcagatcatgcttgaatctctgaaagcactctgaaagatcttctctgttcaagggcaacgctgcg	2950

QY	2941	AGCTTCTCCCGGTGATATACAGACGCTTTTCCGAAGAGATCTTCGAAGCCCTATAACTT	3000
Db	2951	agctctctcccggtctgcatatcacagcttctccgaagagatctctcgaaagctcttcgaagccctatagaagt	3010
QY	3001	TTTTGACACGACCCCCACAGGAGGAGATTCACACAGCTTTTCCAAAGACATGATGAAGT	3060
Db	3011	tttggacagaccccccaaggaagagatcttccaaagagtttccaaagacatgaaagagtc	3070
QY	3061	TGACGTGCGGGCTGCCGTTTCCAGGCGCAGAGATGTTTCATATCCAGAACGTTATCTGCTGTTCTT	3120
Db	3071	tgacgtgctgctgcgtctccagccgagatgctcatccagaaagcttatccgttactcttcgtctctc	3130
QY	3121	CTGTGCTGGGAATGATCGCAGAGACTTTCGCCGTGTTCTTGTGGCAGTGGGGCCCTTGTCT	3180
Db	3131	ctgtgtgggaatgatctcgcaagagatctcccgctgtgtctctcttgcagatgcagtgaggccctctgt	3190
QY	3181	CATCTCTTTTTCACCTCTTGCACTATGTCCTCAGGGTCGTCGATTCGGGAGCTTAACCGCTCT	3240
Db	3191	catctctcttcaagctccgtcacatgctctcccaaggtcccgatcttcgggaagcgcgaagcgctc	3250
QY	3241	GGACAAATATCACGAGAGTCACACTTTCCTTCCTCCACATCACAGTCCTACACATACAGGCGCTTGC	3300
Db	3251	ggacaatatcacgagtcacactctctctctcccaatcacgctcagcatacaagcgctctgc	3310
QY	3301	CACCATCCAGCCCTACAAATAAAGGCGAGATTTCGCAACAGATACACAGAGCTCTGGA	3360
Db	3311	caccatccacgcctacaataaaggcagaggttctctgcacagatcacaggaagctgtctga	3370
QY	3361	TGACAAACAGCTCCCTTTTGTGTTTACGTGCTGGATGCGGTGGCGTGGCGTGGCGGCT	3420
Db	3371	tgaacaacaagctctcttcttcttctgttcaagtgatgcagtgagcgctgcgtctgcgtgc	3430
QY	3421	GGACCTCATGAGCATCGCCCTCATACCAACAGGGGCTGATGATCGTTCTTATACACAGC	3480
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QY	3481	GCAGATTCCCCAGCCCTATGCGGGGTCTCGCATCTCTATATGCTGTCCAGTTAACGGGCT	3540
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Db	3551	gttccagtttaccgctcagactgtgcattgcagaagaagctgcattcaactcgttgagag	3610
QY	3601	GATCAATACACTAATTAAAGCTCTGTGCTTTGGAGAACCTGGCAGATAATTAAACAAAGC	3660
Db	3611	gatacaatacaatacaatlaaagactctgtctcttgaaagacactccagaaatlaaagaaagagc	3670
QY	3661	TGCCCTCCCTGACAGGCCCCAGAGAGGAGAGCGATCTTGGAGACGACAGATAGAGTA	3720
Db	3671	tcctctccctgactgcgcccaggaagagagatgtacacttctggaaacgcagagatgaagta	3730
QY	3721	CCGAGAAAACCTCCCTCTGCTCTCTAAAGAAAGTATCTTACAGATCAAACTTAAAGAA	3780
Db	3731	ccgagaaaacctccctctctgtctctaaagaagatattcttcaagatcaaaacctaaagaa	3790
QY	3781	GATTGGCATTTGTGGGGGCGACAGAGATCGAGGAAGTCTCGCTGGGGATGCGCTTCTCCG	3840
Db	3791	gatttgcatttctgttgcgagacagatcagaagagttctctgccttgcgttgcgtccctcttcg	3850
QY	3841	TCTGTGTGAGATTATCTGAGAGCGCATCAAGATTGTGTGAGTGAAGTCAAGTCAAGTAAATGG	3900
Db	3851	tcgtgtgtgattatctcgtgagagctgcacacaagatctgttgagtgagaaatcagtgatattgg	3910
QY	3901	CCTTGCGAGCTCCGAAAGCAAACTCTATATCTTCATATCCCTCAAGACCGGCTGTTCAATGG	3960
Db	3911	cccttgcgacctccggaagcaactctatcatctctcaagaagccggtgcgtctcaagtg	3970
QY	3961	CACGTGTAGATCAAAATTTGGACCCCTTTCACAACAGTACACTGAAACCGAGATTTGGAGTGC	4020
Db	3971	cactgtatagatcaaatcttggaccccttcaacagatcaccttgaagccagatcttggagctgc	4030

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OY 4021 CCTGAGAGACACACATGAATGATATGCTACGCTACCTGAACTTGAATCTGA 4080
DB 4031 cctgagagagacacacatgaatgatatgctacgctacctgaaactgaaactcga 4090
OY 4081 AGTGTAGGAATGGGGATTAAGTCTCACTGGGGAGACGACCTCTTGCTAGTAG 4140
DB 4091 agtgtatggaatggggatgaatgctcaactggggagacgacacctcttgctagtag 4150
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OY 4201 AGAGACAGACTTATGATTTCAAGAGACCATCCGAGAGATTTGCGACTGTACCTGCT 4260
DB 4211 agagacagacttatgattgattcaagagacccctcgagagagatctgcagactgaaacctc 4270
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DB 4570 tggcttgtgtcttcaacttttgggagagtcataatttgaattatgtatttcttcttcttcttct 4629
OY 4621 TCATGTAACAAATTTAGTTTCTTTCTTAATTCGACTCTTAAAGTTTCAGGAAACGT 4680
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OY 4681 TATTATATTTATGAGAGCGCTTATGATGAGCTTATACGCTTATACGCTTATACCTATAT 4740
DB 4690 tattataatttataagagcgcttataatgaagcttatacagctgagcatalctataat 4749
OY 4741 AATTCGTACATAGCCTATATTTTACAGTGAATAATGTAAGCTGTTTATTTTATTTAAAT 4800
DB 4750 aatctgtacatagcctatatttaccagtgaaatgtaagctgttattattataataat 4809
OY 4801 AAGCACTGTGCTAAAAAA 4819
DB 4810 aagcactgtgctaaaaa 4828

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RESULT 6
US-60-313-371-205

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; Sequence 205, Application US/60313371
; GENERAL INFORMATION:
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Malsen, Gareth
; APPLICANT: Townley, David
; APPLICANT: Morris, MacDonald
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated with ADME Genes
; FILE REFERENCE: EX-0013-5 P
; CURRENT APPLICATION NUMBER: US/60/313, 371
; NUMBER OF SEQ ID NOS: 2447
; SOFTWARE: PERL Program
; SEQ ID NO 205
; LENGTH: 5838

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GB: AF104942
US-60-313-371-205

Query Match      98.9%; Score 4792.6; DB 70; Length 5838;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4809; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

OY 1 GCGTCAATGCTGGAGACCGTGTGACCGCTGCGCGCTTCTCTGACAGAGGCGCCAG 60
DB 11 gctcatgtctcggagagcgtgtgtgtgagcggctggtcgttctcgtgagcagggcgacg 70
OY 61 GAATTTGATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 120
DB 71 gaatttgaatgtaagtaagtaagtaagtaagtaagtaagtaagtaagtaagtaagtaag 130
OY 121 GGATATCGACATAGGAAAAGATATATCATCCCACTCTGGGTATAGAACTGTAGAGGA 180
DB 131 ggatatacgacatagggaaaagatataatcatcccaactctgggtatagaactgtagagga 190
OY 181 GGAACACACACTTCTGGGAGCAGCAGACAGACAGTGTGAAGTTCCAACTTGAAGAACTCG 240
DB 191 ggaacacacacttctgggagcagcagacagacagacagacagacagacagacagacagac 250
OY 241 ACCGTTGGAATGCCAAGATGCTTGGAAACAGACAGCGCGAGCGAGGCGCTCTCTCTGA 300
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OY 301 TGGCTTCATGATTCCTGACGCTCAGAAATCCTGTGATGAGAGCATCCCAAGGAAATACCA 360
DB 311 tggcttcatagtatcctgacgctcagaaatcctgtgatgagagcatcccaaggaaatacca 370
OY 361 TCATGGCTTGAATGCTGCTGTAAGCCATCCGAGACTTTCGAAACACACACACACAGTGA 420
DB 371 tcatggcttgaatgctgctgtaagcccatccgagacttctcgaacacacacacacagtgaga 430
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DB 431 caatgctgggcttctctctgatagaacttctcgtgacttctctctctctctctctctctctct 490
OY 481 CCACAAGAAAGGGGAGCTCTCAATGGAAGACGTGTGTCTGTCTCCAAACAGACAGTCTTC 540
DB 491 ccacaagaaaggaggagctctcaatggaaagacgtgtgtctgtctccaaacagacagactcttc 550
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DB 551 tgaagtgaacctgacagactgagagactgtggcaagagagctgaatgagttgggccc 610
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DB 611 agacgctcttccctgcgaaagggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 670
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DB 791 gctgggctctctgagagaaatgctgcggtctgctgctgctgctgctgctgctgctgctgctgct 850
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DB 851 gaatttacgaaccggtgtctgctggggagcaatcttaacatgacatTTTAAGAAAGAT 910
OY 901 CCTTAAGTTAAGAACTTAAGAAAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960

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Db	911	cottaagtaagaacatctaagaagaatccctcggtgagctcaccataacattgtccaa	970
OY	961	CGATGGCAGAGAATGTTTGGAGCAGCAGCGGTTGGCAGCCTCGCTGGGAGACCCCT	1020
Db	971	cgatggagagaagaattgtttgagagagacgcttggagacgtctgctgagagaccgt	1030
OY	1021	TGTTGCCATCTTAGGCATGATTTATATGTAATTAATTCTTGGACCAACAGCTTCTGGG	1080
Db	1031	tgttgccatcttaggcattgtattataatgttaattatcttggacccaadgagcttcctggg	1090
OY	1081	ATCAGCCTGTTTTTTCCTTTTACCCGAGAATGANTGTTGGATTCACAGGCTCACACATA	1140
Db	1091	atcagcctgttttttccctctttaccaccaaatgattgttgcatacaggtccacagcata	1150
OY	1141	TTTTAGGAAATAATCGCTGGCGCCGACGAGTGAACGTTCCACAAATGATGAATGAAATGTT	1200
Db	1151	tttcaggaagaataatgctgtgcccgaagatgaacgtgtccagaagaatgaatgaattct	1210
OY	1201	TACTTTCATTTAAATTTATCAAAATGTATGCTGGGTCAAAAGCTTTTTCAGAGTTGTTCA	1260
Db	1211	tacttacttaattatccaatatgtatgctgtgttcataaagcatcttccagatgttca	1270
OY	1261	GAAATCCGCGAGAGAGAGCGGTGGGATTTGGAAAAACCCGGGTACTTCCAGACATCAC	1320
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Db	1451	catgacttttgctttgaagaataaacccgctttcagtaaaagtcctccacgaagccctcagt	1510
OY	1501	GGCTGTGACGATTTTAAAGGTTTGTTTCAATGGAAGAGGTTCCACATGATATAAGACAA	1560
Db	1511	ggcgtgtgacgatttaagaagtttgttctcaatggaagaggttccacatgataagaacaa	1570
OY	1561	ACGACGAGTCTTCATCATCAAGATAGAGATGAATAAATGGCACCTTGGCATGGACCTCC	1620
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OY	1621	CCACTCCAGTATCCAGAATCTGGCCCAAGCTGACCCCCAAAATGTAAAAAAGACAAAGGGC	1680
Db	1631	ccaactcagtatccaagaactcgcaccaagctgacccccaatatgnaaaaagacaagaagggc	1690
OY	1681	TTTCAGGGGCAAGAAAGAAAGAGGTGAGGCGACGCTGCAGCGCATCGACATCAGCGGTGCT	1740
Db	1691	tttcaggggcaagaagaagaagaagltgaggcagctgcagcgcacatgacacagcggtgtct	1750
OY	1741	GGCAGACAGAAAAGGCGACCTCTCTCTGACATGACAGAGCGGCCGACGTCGGAAGAGA	1800
Db	1751	ggcagagcagaagaagccactctctctgtgacagltgacgagcggtccagctccggaagagga	1810
OY	1801	AGAAAGCAAGCACATCCACTCTGGGCCACCTGCGCTTACAGAGGACACTCCACAGCATCGA	1860
Db	1811	agaagcagaacacatccaactctggtgcccactgcttacaagaggacacctgcacagcatcga	1870
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Db	1871	ttctggaaatccaagaaggtaaaactggtgtgtaactctgcgcaggtgtgtggaagtgtgaaaac	1930
OY	1921	CTCTCTCATTTACACCAATTTTAGCGCAGATGAGCGCTTTCAGAGGCGACGATTCGAATACG	1980
Db	1931	ctctctcatctttagccattttaggtccaagatgaacgcttccagaaggaagatgtgcaatcag	1990
OY	1981	TGGAACCTTCGCTTATGTGGCCACGACGAGCGTGGATCTCAATGCTACTTACAGAGACAA	2040

D	b	1991	tgrnaactctgcgtatctatgtctgcccgaagccgctggtatccctcaatctgtactctctgaaagaaa	2030
O	y	2041	CATCCTGTTTGGGAAGAAATATGATGAGAAAGATCAACTCTGTCTGAACGCTGCTG	2100
D	b	2051	catccctgtttgggagaagaataatgataigaaagaagatacaactctgtctgtgaagaagctgtc	2110
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D	b	2111	ccctgagccctgacctgtccattctctccagcagcgacctgagcattgagagcagcagc	2170
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D	b	2171	agccaacctgagcggctggcagcgccaagaggaacagccttgcgcggcgctctgtataagta	2230
O	y	2221	CAGAGAGATCTACATCCTGTGACGACGCCCTCACTGGCTTATGATGGCCATGTGGCAACA	2280
D	b	2231	caggaagcatctacatccctgtgaagacccctcagctgacctatgacctatgtgtggcaacca	2290
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D	b	2291	catctcaatagtgctatccggaagaacatctcaagctccaagacagctctgttgttaccaca	2350
O	y	2341	CCAATTACAGTACCTGTTTACTCTGTATGATGAATGATCTTCAATGAAAGAGGCTGATTAC	2400
D	b	2351	ccagttacagtaacctgtgttacctgtatgaagtgtacattctcatgaaagagcgtgtattac	2410
O	y	2401	GGAAGAAGGCAACCCATGAGGAAGTGTAAATGGTGTACTATGCTACATTTTAA	2460
D	b	2411	ggaagaagcgcccaatgaagaaactgtatctaaatgtgtactatgtacacattttaa	2470
O	y	2461	TAACTTGTGCTGGAGAGACACCGCCAGTTGAGATCAATTCAAAAGAAAGAACCACTGG	2520
D	b	2471	taacctgtgtctggagagagccacgcgcagctgtatgatacaatctcaaaaagaaacagcgtg	2530
O	y	2521	TTCCACAGAGAAGTCAACAGACAGGGCTCTTAAACAGSATTCAATTAAGAAAGAAAAAGC	2580
D	b	2531	ttccacagaagaatgcaacaagaacaaggtctcttaaaacagatcatgaaagaagaaaaagc	2590
O	y	2581	AGTAAACCGCAGAGGAAGGAGCTTGTGCAAGCTGGAAAGAAAGGCGAGGGTTCAGTCC	2640
D	b	2591	agtaaaagccagaaagaaagcagctgtgtgaagctgtgaagaaagaaagcagcgtgtcc	2650
O	y	2641	CTGTCTAGTATATGCTGTCTACATCTCCAGGCTGCTGGGGGCCCTTGGCATTCGTGTTAT	2700
D	b	2651	ctgttcagatatagtgtgtctactcctcagcgtctgtgtggggcccttggcatctccgtttat	2710
O	y	2701	TATGGCCCTTTTCATGCTGATGTAGGAGCAACCGGCTTCAGACACCTGTGTGTAAGTTA	2760
D	b	2711	tatggcccttttcatgtgtgaatgttaggcagccgcttcagcacctgtgtgtttagtta	2770
O	y	2761	CTGATTAACGCAAGGAAGCGGGAACACACTGTGACTCGAGGGAAACGAGACCTGGGTGAG	2820
D	b	2771	ctgtataagcaaggaagcgggaacacacactgttgactcgaaggaacgagacctcgtgtag	2830
O	y	2821	TGACAGCATTAAGACAAATCTCATATGCAAGTACTATCGACACATCTACGCCCTCTCCAT	2880
D	b	2831	tgaacagatgaagaaagacaatctctcatatgtacgtactatgtccagcatctcagccctctcat	2890
O	y	2881	GGCAGTCATGCTGATCTCTGAAGCCATTGAGAGAGTTGTCTTGTCAAGGGCACGCTCGC	2940
D	b	2891	ggcagtcatagtcatccctgaagccatctgagaggtgtgtcttltgtcaagggcacgcgtgcg	2950
O	y	2941	AGCTTCTCCCGCTGCTGATGACGAGGTTTCCGAAGATCCTTTCGAACCCCTATGAAGTT	3000
D	b	2951	agcttctcccgctgtcatgaacagcttltccgaagatcccttgcgaacccctatgaagtt	3010
O	y	3001	TTTTGACAGACCCCCACAGAGGAGGATTTCTCAACAGGTTTCCAAAGACATGAGTGAAGT	3060
D	b	3011	ttttgacagacccccacagaggaggtctctcaacaggttlttccaagacatgtagtaagt	3070
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D	b	3071	tgaagtcgagctgccttccaaagccaaagatgttcatctcgaaacatctatccctgtatctct	3130

QY 3121 CTGTGGGAATGATGCGAGAGACTCTCCCGTGTCTTGTGCGAGTGGGGCCCTTGT 3180
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Db 4810 aagcactgtgtaataaca 4828

RESULT 7
US-08-843-459-1
Sequence 1, Application US/08843459
GENERAL INFORMATION:
APPLICANT: SHYJAN, Andrew
TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tesla, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,459
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PENTON, Gillian M
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIL-001

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE: CDS
NAME/KEY: 2..4360
LOCATION: 1
US-08-843-459-1

Query Match 98.5%; Score 4775.4; DB 12; Length 4781;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4773; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

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1927 CATTTAGCCATTTTAGCCAGATGACGCTTCTAGAGGCGAGCATTCAGATGAGAAC 1986
1861 CATTTAGCCATTTTAGCCAGATGACGCTTCTAGAGGCGAGCATTCAGATGAGAAC 1920

QY	1987	CTTCGCTTATGTGGCCCGACAGAGCCCTGGATCTCTCATGTACTCTGTGAGACAACATCCT	2046
Db	1921	CTTTCGCTTATGTGGCCCGACAGAGCCCTGGATCTCTCATGTACTCTGTGAGACAACATCCT	1980
QY	2047	GTTTGGGAAGAAATATGATCAGAAAATATCAACTGTGTCTGAACAGCTGTGCCCTGAG	2106
Db	1981	GTTTGGGAAGAAATATGATCAGAAAATATCAACTGTGTCTGAACAGCTGTGCCCTGAG	2040
QY	2107	GCCTGACCTTGGCCATTTCTTCCAGACAGACCTGACAGGAATTTGGAAGCAGAGGCCAA	2166
Db	2041	GCCTGACCTTGGCCATTTCTTCCAGAGACAGACCTGACAGGAATTTGGAAGCAGAGGCCAA	2100
QY	2167	CCTGAGCGGTGGCGACGCGCCAGAGATCAAGCTTGTGCCCGGACCTTGTATGTGACAGAG	2226
Db	2101	CCTGAGCGGTGGCGACGCGCCAGAGATCAAGCTTGTGCCCGGACCTTGTATGTGACAGAG	2160
QY	2227	CATCTACATCTCTGAGAGACCCCTCAGTGGCTTAGATGGCCCATGTGTGGGCAACCATCTT	2286
Db	2161	CATCTACATCTCTGAGAGACCCCTCAGTGGCTTAGATGGCCCATGTGTGGGCAACCATCTT	2220
QY	2287	CATATGTGCTATCCGGAACATCTCAAGTCCAGACAGATCTGTGTGTTTACCAACAGTT	2346
Db	2221	CATATGTGCTATCCGGAACATCTCAAGTCCAGACAGATCTGTGTGTTTACCAACAGTT	2280
QY	2347	ACAGTACTGTGTTGACTGTGTATGAAGTATCTTCATGAAGAAGGGGTGTATTCAGGAAG	2406
Db	2281	ACAGTACTGTGTTGACTGTGTATGAAGTATCTTCATGAAGAAGAAGGGGTGTATTCAGGAAG	2340
QY	2407	AGGCACCCATGAGAGAACTGATGAATTTAAATGGTACTATGCTTACACATTTTAAATACCT	2466
Db	2341	AGGCACCCATGAGAGAACTGATGAATTTAAATGGTACTATGCTTACACATTTTAAATACCT	2400
QY	2467	GTGTGCTGGAGAGACACCCGACAGTTGAGATCAATTTCAAAAAGGAACCAAGTGGTCCAC	2526
Db	2401	GTGTGCTGGAGAGACACCCGACAGTTGAGATCAATTTCAAAAAGGAACCAAGTGGTCCAC	2460
QY	2527	GAAAGATCACAAGACAAAGGGTCTTAAACAGAGATCAATTAAGAAAGGAAGAACAGTAA	2586
Db	2461	GAAAGATCACAAGACAAAGGGTCTTAAACAGAGATCAATTAAGAAAGGAAGAACAGTAA	2520
QY	2587	GGCAGAGGAAGGGGACACTTGTGACGTGCGAAGAAAGGCGAGGGTTCAAGTGGCTGTGTC	2646
Db	2521	GGCAGAGGAAGGGGACACTTGTGACGTGCGAAGAAAGGCGAGGGTTCAAGTGGCTGTGTC	2580
QY	2647	AGTATATGCTGTCTACATCCAGAGCTCTGTGGGGCCCTTGGCAATCCTGTTATTTATGGC	2706
Db	2581	AGTATATGCTGTCTACATCCAGAGCTCTGTGGGGCCCTTGGCAATCCTGTTATTTATGGC	2640
QY	2707	CCTTTTCATGTGTAATGTAGGACGACCGCCCTTCAGACACCTGTGTGTTAGTACTGAT	2766
Db	2641	CCTTTTCATGTGTAATGTAGGACGACCGCCCTTCAGACACCTGTGTGTTAGTACTGAT	2700
QY	2767	CAGAAGGAACCGGGAAACCACTGTGACTCGAGGGAAACGAGACCTCGGTGAGTGACAG	2826
Db	2701	CAGAAGGAACCGGGAAACCACTGTGACTCGAGGGAAACGAGACCTCGGTGAGTGACAG	2760
QY	2827	CATGAAGCAATCTCTCATATGCAGTACTAGTCCAGACATCTAGGCCCTTCCATGGCACT	2886
Db	2761	CATGAAGCAATCTCTCATATGCAGTACTAGTCCAGACATCTAGGCCCTTCCATGGCACT	2820
QY	2887	CATGCTGATCTCTGAAGAACCATTGAGAGATTTCTTTTGTCAAGGGCAGCCTCGAGCTTC	2946
Db	2821	CATGCTGATCTCTGAAGAACCATTGAGAGATTTCTTTTGTCAAGGGCAGCCTCGAGCTTC	2880
QY	2947	CTCCCGGCTGCATGACGAGCTTTTCCGAAGATCTTTCGAGAGCCCTATGAAAGTTTTTTGA	3006
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QY	3007	CACGACCCCCACAGGAGAGATTTCTAAAGATTTTCCAAAAGCATGAGATGAGATTGAGCT	3066
Db	2941	CACGACCCCCACAGGAGAGATTTCTAAAGATTTTCCAAAAGCATGAGATGAGATTGAGCT	3000

QY	3067	GGGCGCGCGCTTCAGAGCCGAGATGTTCAATCCAGAACGTTATTCCTGCTGTCTCTCTGTCT	3126
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QY	3127	GGGAAATGATCGCAGAGAGTCTCCCGTGTTCCCTGTGAGGAGTGGGGCCCTTGTCATCCT	3186
Db	3061	GGGAAATGATCGCAGAGAGTCTCCCGTGTTCCCTGTGAGGAGTGGGGCCCTTGTCATCCT	3120
QY	3187	CTTTTCAGTCTCTGCACATGTGTCTCCAGGGTCTGATTGGGGAGCTGAACGCTGTGAGACA	3246
Db	3121	CTTTTCAGTCTCTGCACATGTGTCTCCAGGGTCTGATTGGGGAGCTGAACGCTGTGAGACA	3180
QY	3247	TATCAGGAGTACCTTTCTCTCCCAATACATCAGTCCAGCATACAGGGCTTGCCACAT	3306
Db	3181	TATCAGGAGTACCTTTCTCTCCCAATACATCAGTCCAGCATACAGGGCTTGCCACAT	3240
QY	3307	CCACGCGCTACAAATAAAGGGCAGAGTGTGTGACAGATACCGAGAGCTGTGATGAGACA	3366
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QY	3367	CCAAGCTCCTTTTTTTTTTTGTGTACGTGTGCGATGCGGTGGCTGTGCGGCTGGACCT	3426
Db	3301	CCAAGCTCCTTTTTTTTTTTGTGTACGTGTGCGATGCGGTGGCTGTGCGGCTGGACCT	3360
QY	3427	CATCAGACATCCGCTTCATATACCAACACAGGGGCTGATGATGTTCTTATATGACAGGGCAGAT	3486
Db	3361	CATCAGACATCCGCTTCATATACCAACACAGGGGCTGATGATGTTCTTATATGACAGGGCAGAT	3420
QY	3487	TCCCCGAGCTTATGGGGGCTCGGCATCTATAGCTGTCCAGTTAACGGGGCTGTTCGA	3546
Db	3421	TCCCCGAGCTTATGGGGGCTCGGCATCTATAGCTGTCCAGTTAACGGGGCTGTTCGA	3480
QY	3547	GTTTACGCTCAGACTGGCATCTGAGACAGAAAGCTGATTCACCTCGGTGGAGAGATCAA	3606
Db	3481	GTTTACGCTCAGACTGGCATCTGAGACAGAAAGCTGATTCACCTCGGTGGAGAGATCAA	3540
QY	3607	TCACATACATTAAGACTCTGTCTCTTGGAAAGCACCTGCCAGATTTAAGAACAAAGGCTCCCTC	3666
Db	3541	TCACATACATTAAGACTCTGTCTCTTGGAAAGCACCTGCCAGATTTAAGAACAAAGGCTCCCTC	3600
QY	3667	CCCTGACTGGCCCCCAGGAGGGAGAGTACCTTTAGAACCAAGAGATGAGTACCCGGA	3726
Db	3601	CCCTGACTGGCCCCCAGGAGGGAGAGTACCTTTAGAACCAAGAGATGAGTACCCGGA	3660
QY	3727	AAACCTCCCTCTGCTCTAAAGAAAGTATCCCTTCACGATCAAACTAAAGAGAGATTTGG	3786
Db	3661	AAACCTCCCTCTGCTCTAAAGAAAGTATCCCTTCACGATCAAACTAAAGAGAGATTTGG	3720
QY	3787	CATTTGTGGGGCGGACAGGATCAGGGAATCTCGCTGGGGATGGCCCTCTTCCCTGTGGT	3846
Db	3721	CATTTGTGGGGCGGACAGGATCAGGGAATCTCGCTGGGGATGGCCCTCTTCCCTGTGGT	3780
QY	3847	GGAGTTATCTGGAGCTGCATCAATGAATGATGGAGTGAATCAATGATTTGGCCCTTGC	3906
Db	3781	GGAGTTATCTGGAGCTGCATCAATGAATGATGGAGTGAATCAATGATTTGGCCCTTGC	3840
QY	3907	CGACCTCCGAAGCAAACTCTATCATCTCTCAAGAGCGGGTGTCTCAAGTGCACACTGT	3966
Db	3841	CGACCTCCGAAGCAAACTCTATCATCTCTCAAGAGCGGGTGTCTCAAGTGCACACTGT	3900
QY	3967	CAGATCAAAATTTGGACCCCTTCAACCAAGTACAGTGAAGACCAGATTTGGAGTCCCTGGA	4026
Db	3901	CAGATCAAAATTTGGACCCCTTCAACCAAGTACAGTGAAGACCAGATTTGGAGTCCCTGGA	3960
QY	4027	GAGGACACACATGAAAGAAATGTATTTGGCAGCTACCTCTGAACTTAATCTGAAGAT	4086
Db	3961	GAGGACACACATGAAAGAAATGTATTTGGCAGCTACCTCTGAACTTAATCTGAAGAT	4020
QY	4087	GGAGAAATGGGATTAACCTTCTCAGTGGGGGAAACGGCAGCTCTTGATCTAGTACAGCCCT	4146
Db	4021	GGAGAAATGGGATTAACCTTCTCAGTGGGGGAAACGGCAGCTCTTGATCTAGTACAGCCCT	4080
QY	4147	GCTCCGCCACTGTAAAGATCTGTGATTTTAAAGTGAAGCCACAGCTGCCATGAGACACAGAC	4206

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Db 4081 GCTCCGCCACGTAAAGATTCTGATTTAGATGAAGCCACAGCTGCATGACACAGAGAC 4140
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QY 4207 AGCATATTGATTCAGAGAGACCATCCGAGAGAGATTTCAGACTGTACATGCTGACCAT 4266
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Db 4141 AGCATATTGATTCAGAGAGACCATCCGAGAGAGATTTCAGACTGTACATGCTGACCAT 4200
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QY 4267 TGCCCATTCGCTGCACAGCGTTCTAGAGCTCCAGATAGATATGCTGTGACAGGAGACA 4326
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Db 4201 TGCCCATTCGCTGCACAGCGTTCTAGAGCTCCAGATAGATATGCTGTGACAGGAGACA 4260
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QY 4327 GGTGGTGGAGTTTGACACCCCATCGCTCTCTGTCACACAGACAGTTCGCGATTCTATGC 4386
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RESULT 8
US-60-226-176-206
; Sequence 206, Application us/60226176
; GENERAL INFORMATION:
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Malsen, Gareth
; APPLICANT: Townley, David
; APPLICANT: Morris, MacDonald
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated with ADME Genes
; FILE REFERENCE: GX-0013-1 P
; CURRENT APPLICATION NUMBER: US/60/226,176
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2447
; SOFTWARE: PERL Program
; SEQ ID NO 206
; LENGTH: 4314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GB:AF104942.1
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Query Match

88.8%; Score 4304.4; DB 61; Length 4314;

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 4308; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db	781	aagatccctaagttaaagaacataaagaagaatccctggtgtgagctcatcaaatcttgc	840
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 QY 4376 CGATTCTATGCCATGTTTGTGCTGTGACAGAGAACAAGGTCCGCTGCAAGGCTGA 4429
 Db 4261 cgattctatgcattgttctgtcgtgacagagacaaggtcgtcgaaggtctga 4314

RESULT 10
 US-60-313-371-206
 ; Sequence 206, Application US/60313371
 ; GENERAL INFORMATION:
 ; APPLICANT: Ring, Huijun Z.
 ; APPLICANT: Malsen, Gareth
 ; APPLICANT: Tomlley, David
 ; APPLICANT: Morris, MacDonald
 ; TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
 ; FILE REFERENCE: GX-0013-5 P
 ; CURRENT APPLICATION NUMBER: US/60/313,371
 ; CURRENT FILING DATE: 2001-08-16
 ; NUMBER OF SEQ ID NOS: 2447
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 206
 ; LENGTH: 4314
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: GB:AF104942.1
 US-60-313-371-206

Query Match 88.8%; Score 4304.4; DB 70; Length 4314;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4308; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 116 ATGAAGATATCGCATAGGAAGAAAGATATATCATCCCGAGTCTGGGTATAGAAGTGTG 175
 Db 1 atgaagatatcgacataagaaagatatacatcccccagctcctgggtatagaaggtgtg 60
 QY 176 AGGAGAGAACACACACTTCTGTGGAGCCACAGAGACCGGTGAAGATTCCAAGTTTAGAGA 235
 Db 61 aggagagaaacacacttctgtggagcagacagaaacgtgaaggttccaagttcaagaga 120
 QY 236 ACTTGACCGTTTGGATGCCAAGATGCTTGGAAACAGACAGCCGACCGGAGGCTCTCT 295
 Db 121 acttgaccglttggaatgccaagatgaccttggaaacagacccgagccgagggccttct 180
 QY 296 CTGTATGCTTCACATGCTTCTCAGCTCAGATCCTGATGAGAGAGCATCCCAAGGGAAG 355
 Db 181 ctgtatgcttcacatgcttctcagctcagatcctctgataagatcttgagagatcccaagggaag 240
 QY 356 TACCATCATGGCTTGAAGTCTGTAAGCCCATCCGCACTACTTGCAAACACACAGCACCA 415
 Db 241 taccatcatggttgaagtctgtgaagcccatccgactacttccaacaccagcacca 300

OY	416	GTGACAAATGCTGGCGCTTTTTCCTGTGATGACTTTTTCGTGGCTTTCCTCTGTGGCCGT	475
Db	301	GTGAGCAATGCTGGCGCTTTTTCCTGTGATGACTTTTTCGTGGCTTTCCTCTGTGGCCGT	360
OY	476	GTGGCCCAACAGAAAGGGGAGACTTCATATGGAAGAGCTGTGGTCTGTGCCAAGCAGAG	535
Db	361	GTGGCCCAACAGAAAGGGGAGACTTCATATGGAAGAGCTGTGGTCTGTGCCAAGCAGAG	420
OY	536	TCTTCTGACGTAAGTCACTCAGAAAGACTGTGAGAGACTGTGGGAGAAAGACTGTAACTGT	595
Db	421	TCTTCTGACGTAAGTCACTCAGAAAGACTGTGAGAGACTGTGGGAGAAAGACTGTAACTGT	480
OY	536	GAGCGACAGCTGTCTCCCTGCGAAGGGTGTGTGGATCTTCTGCGACACAGGCTCATC	655
Db	481	GAGCGACAGCTGTCTCCCTGCGAAGGGTGTGTGGATCTTCTGCGACACAGGCTCATC	540
OY	656	CTGTGCATCGGTGTGCGGTGATGATACGACGAGTGGCTGCTTCAGTGGACCAAGCTTCATG	715
Db	541	CTGTGCATCGGTGTGCGGTGATGATACGACGAGTGGCTGCTTCAGTGGACCAAGCTTCATG	600
OY	716	GTGAAACACCTTGTGGAGTATACCAAGGCAACAGACTCAACCTGGAGACAGCTTGTG	775
Db	601	GTGAAACACCTTGTGGAGTATACCAAGGCAACAGACTCAACCTGGAGACAGCTTGTG	660
OY	776	TTTAGTCTGGGCGCTCTCTGACGGAATCTGGGCTTGTGGTGGCTGTGACATGACTTGG	835
Db	661	TTTAGTCTGGGCGCTCTCTGACGGAATCTGGGCTTGTGGTGGCTGTGACATGACTTGG	720
OY	836	GCATTGATTTACCAACCGGTGTCCGTTCGGGGGGCCATCTTAACATGGCATTTAAG	895
Db	721	GCATTGATTTACCAACCGGTGTCCGTTCGGGGGGCCATCTTAACATGGCATTTAAG	780
OY	896	AAGATTCCTTAAGTAAAGAACATTAAAGAAATCCCTGGGAGAGCTATCAACTTTGC	955
Db	781	AAGATTCCTTAAGTAAAGAACATTAAAGAAATCCCTGGGAGAGCTATCAACTTTGC	840
OY	956	TCCAAACGATGGCGAGAAATGTTTGAAGCAGCACCCGTTGGCAGCTGTGGCTGAGAGA	1015
Db	841	TCCAAACGATGGCGAGAAATGTTTGAAGCAGCACCCGTTGGCAGCTGTGGCTGAGAGA	900
OY	1016	CCCCGTGTGCGATCTTAAGCATGATTTATATGTAATTTCTGGAGCAACAGGCTTC	1075
Db	901	CCCCGTGTGCGATCTTAAGCATGATTTATATGTAATTTCTGGAGCAACAGGCTTC	960
OY	1076	CTGGGATCAGCTGTTTTTATCTCTTTCCTTACCCGCAATATGTTTGGCATCAGGCTGCA	1135
Db	961	CTGGGATCAGCTGTTTTTATCTCTTTCCTTACCCGCAATATGTTTGGCATCAGGCTGCA	1020
OY	1136	GCATATTTTCAGAGAAATCGTGGCGCCGACGAGTGAACGTGTCCAGAAAGTATGATNA	1195
Db	1021	GCATATTTTCAGAGAAATCGTGGCGCCGACGAGTGAACGTGTCCAGAAAGTATGATNA	1080
OY	1196	GTTCTTACTTACATTAATTTATCAAAATGTATGCTGGGTCAAAGCATTTTCTCAGAGT	1255
Db	1081	GTTCTTACTTACATTAATTTATCAAAATGTATGCTGGGTCAAAGCATTTTCTCAGAGT	1140
OY	1256	GTTTCAGAAATCCGCGAGGAGGAGAGCTGCGATTAATGGAAAGACCGGGTACTTCCAGAGC	1315
Db	1141	GTTTCAGAAATCCGCGAGGAGGAGAGCTGCGATTAATGGAAAGACCGGGTACTTCCAGAGC	1200
OY	1316	ATCACTGTGGGTGGGCTCCCATTTGTGTGATTTGACAGGTGGTGAACCTTCTGCTT	1375
Db	1201	ATCACTGTGGGTGGGCTCCCATTTGTGTGATTTGACAGGTGGTGAACCTTCTGCTT	1260
OY	1376	CATATGACCTGGGCTTCGATCTGACAGCAGACAGGCTTTCACAGTGGTGAAGCTTC	1435
Db	1261	CATATGACCTGGGCTTCGATCTGACAGCAGACAGGCTTTCACAGTGGTGAAGCTTC	1320
OY	1436	AATTCATGACTTTTGTTTGAAGATTAACACCGTTTCACTAAAGTCCCTCTCAAGAAC	1495
Db	1321	AATTCATGACTTTTGTTTGAAGATTAACACCGTTTCACTAAAGTCCCTCTCAAGAAC	1380

QY	1496	TCAGTGGCTGTTTGACAGATTTTAAAGTTTGTCTTAATGGAAGAGGTTACACTGATTAAG	1553
Db	1381	TCAGTGGCTGTGTGACAGATTTTAAAGTTTGTCTTCTTAAATGGAAGAGGTTACACTGATTAAG	1440
QY	1556	AACCAACCAAGCAGGCTTCATCATCAATGAGATGAGATGAAAAATGGCAACCTTGGCATGGGAC	1615
Db	1441	AACCAACCAAGCAGGCTTCATCATCAATGAGATGAGATGAAAAATGGCAACCTTGGCATGGGAC	1500
QY	1616	TCCCTCCGACTCCAGTATTCAGCAATCCGCCACACTGACACCCCAAAATGTAAAAAGCAG	1675
Db	1501	TCCCTCCGACTCCAGTATTCAGCAATCCGCCACACTGACACCCCAAAATGTAAAAAGCAG	1560
QY	1676	AAGGCTTCAGAGGGCAGAAAAAGAGAGTGTAAGCAGCTGCAGCCACTGACATACAGGC	1735
Db	1561	AAGGCTTCAGAGGGCAGAAAAAGAGAGTGTAAGCAGCTGCAGCCACTGACATACAGGC	1620
QY	1736	GTGCTGGCAGAGCGAAAAAGGCGACCTCTCTGTGACAGTAGAGAGGGCGCGTCCGAA	1795
Db	1621	GTGCTGGCAGAGCGAAAAAGGCGACCTCTCTGTGACAGTAGAGAGGGCGCGTCCGAA	1680
QY	1796	GAGGAAGAAGGCAAGCAACATTCACCTGGGCGACCTGCCTTACAGAGACACTGCACAGC	1855
Db	1681	GAGGAAGAAGGCAAGCAACATTCACCTGGGCGACCTGCCTTACAGAGACACTGCACAGC	1740
QY	1856	ATCGATCTGGAGATTCCAAGAGGGTAAACTGTTGGTAATCTGGCGCAGTGGGAAGTGA	1915
Db	1741	ATCGATCTGGAGATTCCAAGAGGGTAAACTGTTGGTAATCTGGCGCAGTGGGAAGTGA	1800
QY	1916	AAAACCTCTTCATTTCCAGCATTTTGGCCGACATGACGCTTCTAGAGGCGACGATTCGA	1975
Db	1801	AAAACCTCTTCATTTCCAGCATTTTGGCCGACATGACGCTTCTAGAGGCGACGATTCGA	1860
QY	1976	ATCAGTGGCAACCTTGCTTATGTGGCCGACAGCGCTGGATCCTCAATGCTACTGTGAGA	2035
Db	1861	ATCAGTGGCAACCTTGCTTATGTGGCCGACAGCGCTGGATCCTCAATGCTACTGTGAGA	1920
QY	2036	GACCAACTCTCTGTTGGGAAGGAATATGATGAAGAAATACACTCTGTGCTGACAGC	2095
Db	1921	GACCAACTCTCTGTTGGGAAGGAATATGATGAAGAAATACACTCTGTGCTGACAGC	1980
QY	2096	TGCTGCTGAGGCGCTGACCTGGGCACTTCCTCCAGCAGGACCTGACGAGATTGGAGAG	2155
Db	1981	TGCTGCTGAGGCGCTGACCTGGGCACTTCCTCCAGCAGGACCTGACGAGATTGGAGAG	2040
QY	2156	CGAGAGGCAACCTTGAGCGGTGGGCGAGCGCGCAAGANTAGCCTTGCCGGGCTTGTAT	2215
Db	2041	CGAGAGGCAACCTTGAGCGGTGGGCGAGCGCGCAAGANTAGCCTTGCCGGGCTTGTAT	2100
QY	2216	AGTGACAGAGCACTTCAACTCTTGAGACAGACCCCTCAGTGCTTAAGTCCCATGTGGGC	2275
Db	2101	AGTGACAGAGCACTTCAACTCTTGAGACAGACCCCTCAGTGCTTAAGTCCCATGTGGGC	2160
QY	2276	AACCAACTCTTCATTAATGCTATCCGAAAACTCACTCACTCCAAAGCAAGTCTCTTTGTT	2335
Db	2161	AACCAACTCTTCATTAATGCTATCCGAAAACTCACTCACTCCAAAGCAAGTCTCTTTGTT	2220
QY	2336	ACCACCAAGTTACAGTACTCTGTTTGAATCTGTAAGTAATTTATTAAGAGAGCGCTGT	2395
Db	2221	ACCACCAAGTTACAGTACTCTGTTTGAATCTGTAAGTAATTTATTAAGAGAGCGCTGT	2280
QY	2396	ATTACGGAAGAAGGCAAGCCCATGAGGAAGTATGAATTTTAAATGTGACTATGCTACATT	2455
Db	2281	ATTACGGAAGAAGGCAAGCCCATGAGGAAGTATGAATTTTAAATGTGACTATGCTACATT	2340
QY	2456	TTTAAATTAACCTGTGGCTGGGAGAGACACCGCCAGTTGAGATCAATTTCAAAAAGGAACC	2515
Db	2341	TTTAAATTAACCTGTGGCTGGGAGAGACACCGCCAGTTGAGATCAATTTCAAAAAGGAACC	2400
QY	2516	AGTGGTTACAGGAAGAAGTACAAAGCAAGGGGCTCCAAAACGATCAATTAACAAGGA	2575
Db	2401	AGTGGTTACAGGAAGAAGTACAAAGCAAGGGGCTCCAAAACGATCAATTAACAAGGA	2460
QY	2576	AAACAGATTAAGCCAGAGGAAGGCGCTTTGTGACGTGGAAGGAAGAAAGGCGACAGGTTCA	2635

|||||
Db 2461 aagcagtaagccagagagagcctgtgacgtgtaagaagaagggcaggttca 2520
OY 2636 GTGCGCTGTGATATATGATGTGTATCATCCAGGCTGTGGGGCCCTTGGCATTCCTG 2695
Db 2521 gtgcccgtgacgtatatagtgtctacatccaggtctggtggggcccttggcattcctg 2580
OY 2696 GTTATTATGGCCCTTTTCACTGTAATGTATGAGGACCGCCCTTACACACTTGTGTTG 2755
Db 2581 gtattatagcccttctcactgaaatgtagagacgcgcttcagaccctgtgtg 2640
OY 2756 AGTTACTGATCAGCAAGAGAGAGCGGACACACTGTGACTGAGAGGAGACACTGCG 2815
Db 2641 agttactgtgtcaagaaggaagcggaacacacactgtgtcgtgaggaacgagactcg 2700
OY 2816 GTGAGTGACAGCATGGAAGACAAATCCTCATATAGCATATATGCGACATCTACGCCCTC 2875
Db 2701 gtgagttagcagcactgaaggaacatcccatatgacgtactatgtcagcaltcaagccctc 2760
OY 2876 TCCATGGCAGTCATGCTGATCCTGAAAGCATTCGAGAGTGTGCTTGTTCAGAGGCGACG 2935
Db 2761 tccatgagcagtcacgtcgtacccgtgaagccatccgagagttgtcttgcgaagggcagc 2820
OY 2936 CTGCGAGCTTCTCCCGGCTGTCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATG 2995
Db 2821 ctgagagcttccctcccggtcgtacgtgaagactttccgaaagatccttcgaaagccctatg 2880
OY 2996 AAGTTTTTGGACAGACCCCGACAGGAGGATTTCTCAACAGTTTCCAAAGACATGAT 3055
Db 2881 aagtttttggacagaccccgacagagagatctcacaagtttccaaagacatggt 2940
OY 3056 GAAGTTGAGCTGGGGGCGGCTTCAGGGCGAGATGTTTCAAGAGATTCATCCAGATTCCTGCTG 3115
Db 2941 gaagttgagctggggcggttcagggccgagatgttcatccgaagcgtltaaccgtg 3000
OY 3116 TTCTTGTGTGGGAATGATGCGAGAGATCTTCCCGTGTCTTGTGCGAGTGGGGCCC 3175
Db 3001 ttcttctgtgtggaaatgatgcagagagttcccggtgtcttctgtgtgcaagtggtggccc 3060
OY 3176 CTGTGTACTCTCTTTTTCAGTCTGTCGACATTTGTCTCCAGGGTCTTGATCGGAGCTTAAG 3235
Db 3061 ctgtgtactctcttcttcaagtcctgacatgtgtccaggggtccgtgattcggagactgaag 3120
OY 3236 CGTCTGGACATATACAGCGAGTCACTTTCCTCCACATCACTGCTCAGATATACAGGGC 3295
Db 3121 cgtctggacatatcaagcagtcaccttccctccacatcaagtcacagatacaagc 3180
OY 3296 CTTGCCACATCCACGCGCTACAAATTAAGGGCAGAGATTGTGCAAGATACAGAGACTG 3355
Db 3181 ctggccacatccacgctacataaaggcaggaagttctgtgcacagataccaggaagctg 3240
OY 3356 CTGGATGACACACAGCTCTCTTTTGTTTTGTATAGTGTGCGAGTGGGTGGCTGTG 3415
Db 3241 ctggatgacacacagctctcttcttcttcttcttcttcttcttcttcttcttcttcttct 3300
OY 3416 CGGCTGACCTCAATCAGCATCGGCTCATACACACAGGGGGGATGATGCTTCTTATG 3475
Db 3301 cggctgacccatccagcactcgcctccatccacacacaggggctgagatcgttctatg 3360
OY 3476 CAGGGGAGATTCGCCAGGCTATGCGGCTGTGCGCATCTTATGCTGTCCAGTTAAG 3535
Db 3361 caggggagatcccccagcctatcggtgtcgcacatcccttatgtgtccagttacg 3420
OY 3536 GGGCTGTTCAGTTTACGGTTCAGACTGTGACATGTGACACAGAGCTGATTCACCTCGGTG 3595
Db 3421 gggctgttccagttcaggtcagactgtgcatctgaagacaaagctcgtatccactcggtg 3480
OY 3596 GAGAGATCATACTAGATTAAAGACTCTGCTTGAAGACACTGCGACAGATTAAAGAC 3655
Db 3481 gagaagatcatcactaactaagaactcgttcccttggaagaccccgcaaatlaaagac 3540
OY 3656 AAGGTCCTCTCCCTGACTGAGCCCGACAGAGGAGAGGTGACTTTGGAAGACGACAGATG 3715
|||||

Db 3541 aaggtccctccctcctgactgccccagggagggaggtgacctttgagaacgacagagatg 3600
OY 3716 AGGTACCGAGAAAACCTTCCTCTGCTCTTAAGAAATATCTTACAGATCAAACTTAAA 3775
Db 3601 agttaccgagaanaacccctctctgtcttaagaagaatlatccttcaagatcaaacctlaaa 3660
OY 3776 GAGAGATTTGGCATTTGGGGGGGAGACAGATCAAGGAAAGTCTGCTGGGATGAGCCCTC 3835
Db 3661 gagaagatgtgcatctgtgggggagacagatcaaggaagctccgcctggtgggaatggccctc 3720
OY 3836 TTCCGTGTGTGAGTATATCTGAGGCTGCATCAAGATTGATGAGTGAAGATACAGTAT 3895
Db 3721 ttccgtctgtgtgagttatctgtaggtgtcatcaagttgtagtggaggaatcagtgat 3780
OY 3896 ATTGGCTTGGCGACTCCGAGCAAGAACTCTATCATTTCTTCAAGAGCCGGTCTGTTG 3955
Db 3781 attggccttgcgaaccccgaaagaaactctctcatctcctaagaagccggtgtgtc 3840
OY 3956 AGTGGCACTGTGAGATCAAAATTTGGACCCCTTCAACCGATACACTGAAGACCAATTTGG 4015
Db 3841 agtggcaactgtcagatcaaatcttgacccttcaacagatcacctggaagaccagatctgg 3900
OY 4016 GATGCCCTTGAGAGAGACACATGAAGAAATGTAATGCTCAGTACCTCTGAAACTTGA 4075
Db 3901 gatgcccttgagagagacacacatgaaagaatgtatctgctcgaactccttgaacttgaa 3960
OY 4076 TCTGAAGTATGAGAAATGGGGATTACTTCTCACTGGGGGAGCGCAGCTTGTGATA 4135
Db 3961 tctgaagatgtatgagaatgtggaaatctctcagttggtgggaagcgcgcttctgtcata 4020
OY 4136 GCTAGAGCCCTGCTCCGCGCACTGTAAGATTCGTATTTAGATGAAGCACAGCTGCCATG 4195
Db 4021 gctagagccctgtctccgcacactgtaagatctgattatgataagccacagctgcatg 4080
OY 4196 GACACAGAGACAGACTTATTTGATTCAGAGACATCCGAGAAAGATTTGGACACTGTACC 4255
Db 4081 gacacagagacagacttatgtattcaagagacatccgagaagacttgcagactgtacc 4140
OY 4256 ATGTGACATTTGCCCATTCGCTTCACACAGGTTTAAAGTCCGATTAAGATTATGCTGTG 4315
Db 4141 atgtgacatctgtcccatcgccagtcagacaggttctgaagctcagatagatatagtgtcgt 4200
OY 4316 GCCCAGGAGAGGAGTGTGAGATTGACACCCCATCGGTCTTGTGTCACAGACACTTCC 4375
Db 4201 gcccagagagagtggtgtgaggttggacaccccatcggtcttctgttcaacagagatctc 4260
OY 4376 CGATTCTATGCCAGTTTGTGCTGTGACAGAAACAAGGTGCGTGTCAAGGGCTGA 4429
Db 4261 cgattctatgcagtgttctgtcgtcagagagaaggtcgtgtcgaagggtcgtga 4314
|||||

RESULT 11
US-60-324-185-5709
; Sequence 5709, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Tal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 5709
; LENGTH: 5782
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1099526.1

US-60-324-185-5709

Query Match 81.9% Score 3969.6; DB 71; Length 5782;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 4108; Conservative 0; Mismatches 4; Indels 116; Gaps 2;

QY 707 GCCTTCATGTTGAACACACCTCTTGGAGTATACCGACAGCAACAGCTCTAACCTGCAGTAC 766
DB 571 gcttcatagtgtaaacacctcttgagatacccgacagacagatctcaacctgcagtaac 630
QY 767 AGCTTGTTGTTAGTGTGGGCTCTCTCTGACGAAATGTCGGCTGTTGTCGCTGCA 826
DB 631 agcttggtttagtgctggtgctctctctcctgcagaaatcgtagtcttggctgcgttga 690
QY 827 CAGATTGGGCAATGAATTAACGAACCGGTGTCCTGCGGGGGCCATCTTAACCATG 886
DB 691 ctgacttggcattgaataaccgaaccggtgtccgttcggtggggccatcttaaccatg 750
QY 887 GCATTTAAGAAAGATCCTTAAGTTAAAGAAATTAAGAAATCCTGGGTGAGTCATC 946
DB 751 gcatttaagaagatcccttaagtttaagaacatlaaagaatacccttgggtgagctcacc 810
QY 947 AACATTTGCTCCAAACGATGGGACAGAAATGTTGAGGACGACCGTTGGACCTGCTG 1006
DB 811 aacatttgctccaacgactgggacagaaatgtttgagycagcagccgtttggcagctgtcg 870
QY 1007 GCTGAGAGACCCGTTGTTGCCATCTTAAAGCATGATTTATATGTAATTTCTGGACCA 1066
DB 871 gctgagagaccggttgtgcacatcttagcagcatlataatgtaattatcttggacca 930
QY 1067 ACAGGCTTCCTGGAGTACAGCTGTTTATACCTTTTACCCGACATATGTTTGCATCA 1126
DB 931 acaggcttccctggggtacgcgttttatacccttatacccgacgaatgattgtttcacata 990
QY 1127 CGGCTCACGACATATTTGAGAGAAATGCGTGCCGACCGATGAACGTTGCCAGAG 1186
DB 991 cggctcacagacatatttcaggaanaatgctggtgcgcacagatgaacgtgttccagaag 1050
QY 1187 ATGAATGAAGTTTCTACTTAATTAATTTATCAAAATGTAATGCTGGCTCAAGCATTT 1246
DB 1051 atgaatgaagttctacttaataatattcaaaaagtatgcttgggttcaagaatctt 1110
QY 1247 TCTGAGAGTGTTCAGAAATCCGCGAGAGAGAGCGTGGATTTGAAAAAGCCGGGTAC 1306
DB 1111 tctcagagtggttcagaanaataccgagagagagcgctggaatctggaanaaagccgggtac 1170
QY 1307 TTCAGAGCATCAGTGGGTGGGCTCCATTGATGATGATGATGATGATGATGATGATG 1366
DB 1171 ttccagagcatcactgt 1230
QY 1367 TTTCTGTTCATATGACCCCTGGGCTTCGATCTGACAGCAGCAGGCTTTTCAAGTGTG 1426
DB 1231 ttctctgttcatatgacccctgt 1290
QY 1427 ACAGTTCATATTCATGACTTTTGTGAAAGTAACACCGTTTTCGTAAGTCCCTC 1486
DB 1291 acagtttcatatcactgt 1350
QY 1487 TCAGAGAGCTCAGTGGCTGTTGACAGATTTA----- 1517
DB 1351 tcagaagagcctcagtgctgtgacagatttaagcttcttccactgtaagcctgtaagtgtg 1410
QY 1518 ----- 1517
DB 1411 ttgtgctaagtgagtgtaagccctaaggtgttccctgtgtctgtatccagtgtctcacc 1470
QY 1518 -----AGAGTTGTTTCTAATGGAAGGTTTCACATGAT 1551
DB 1471 ttgtgacctctctcacaaactctctcagagttgtttctcaatggaagggtttccacatg 1530
QY 1552 AAAGAACAAACGACCGCTCTCATCAATCAAGATGAGATGAAAAATGCCACTTGGCATG 1611
DB 1552 aaagaaacaaacgacccgacttctcatcaatgaatagaatgaaatgccaacttggcatg 1590
QY 1612 GGAATCTCTCCACTCCAGATATCCAGAACTGCCCAAGCTGACCCCAAAATGAAAAAGA 1671
DB 1591 ggaatctctccactccactcagatctcagaactcgcgaagcttgcaccccaaatgtaaaaaa 1650
QY 1672 CAAGAGGGCTCCAGGGGAGAGAAAGAGAGAGGAGGAGGCTGACGCTGACCTGACATCA 1731
DB 1651 caaagagggctcccaaggaggaagaagaagtgagggcagcttgcagcgacatgaagatca 1710
QY 1732 GCGGCTGCTGGACAGACAGAAAGGCCACCTCTCTGAGACAGTGAAGACGAGCGGCCAGTCC 1791
DB 1711 ggcgtgtctggcagagcagaagaagccaactctctcctgcagcagtgagagcgccagctcc 1770
QY 1792 CGAAGAGGAAGAAAGGACACATCTCACTGGGCCACCTGCGCTTACAGAGCACTGCA 1851
DB 1771 cgaagaggaagaaggaacacatcccaacttggcccaacttgcagtaagagacatctga 1830
QY 1852 CAGCATCGATCTGGAGATCCAGAGAGGCTAACTGCTTGAATCTGCGGCACTGGGAAG 1911
DB 1831 cagcatcgaatctggagatcccaagaaggttaactgtgtgaatcttgcagctgttggagag 1890
QY 1912 TGGAAAAACCTCTCTCATTTCAAGCCATTTTAAAGCAGATGACGCTTCTGAGGAGCAT 1971
DB 1891 tggaaaaacctctctcacttccatcttcagccaattttagccagatgaacgtcttgaagggcag 1950
QY 1972 TGCATCACTGGAACCTTCCTGATTATGTGGCCAGCAGAGCCCTGGATTCATGCTACTCT 2031
DB 1951 tgcaatcagtggaaccttcgcttaltgtggtccagcagcgctgtgaltccatcagctactct 2010
QY 2032 GAGAGCAACATCCTGTTTGGAGAAATATATATGAAGAAATACACTCTGTGTGAA 2091
DB 2011 gagagacaacatccctgttggagaaagaaatgaatgaagaagaatcaactctgtctgaa 2070
QY 2092 CAGCTGCTGCTGAGAGGCTGACCTGGCCATTTCTCCACACGACACTGACGAGATTGG 2151
DB 2071 cagctgctgctgagagcctgacacttgcattcttcccgacagcagacttgcaggaattgg 2130
QY 2152 AGAGCGAGGAGGCAACTGAGCGGTGGGCGAGCGCAGAGATCAAGCTTGGCCGGGCTT 2211
DB 2131 agagcgagaggaagcaaacctgaagcgtgtggagcgacagagatcagccttggccggcctt 2190
QY 2212 GATATGTGACAGAGACATCTACATCTGAGACACCCCTCATGCTTGAATGATGCCATGT 2271
DB 2191 gatatgtgacagagacatctacatcttgcagacacccctcagcttgaatgacctgacatgt 2250
QY 2272 GGGCAACACATCTCAATAGTGTATCGGAAACATGTCAGAGTCAAGACAGTCTGT 2331
DB 2251 gggcaaacacatcttcaatagtgatctatccggaacaatctcaagttcaagacagcttctgt 2310
QY 2332 TGTACCCACAGTTACAGTACCTGCTGATGATGATGATGATGATGATGATGATGATG 2391
DB 2311 tgtlaccacacagttacagttactgtgtgactgtgtgaagtgtgaagttcttcaatgaagaagg 2370
QY 2392 CTGTATTTACGGAAGAGGACCCATGAGGAACCTGATGATGATGATGATGATGATGATG 2451
DB 2371 ctgtattacggaagaaggaagcccaatgaagaaactgtgtgaatlaaactgtgtgactatgtac 2430
QY 2452 CATTTTAAATAACCTGTTGCTGGAGAGACACCGCAGTTCAGATTCATTTCAAAAAAGA 2511
DB 2431 cattttaataaacctgt 2490
QY 2512 AACGAGTGTTCAGAGAAAGTCAAGACAGCAAGGCTCTTAAACAGAGTCAATTAAGAA 2571
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QY	4081	AGGATGAGNAAATGGGGATTAACCTTCACAGTGGGGGAAACGGACGCTCTGTGTGCATAGCTAG	4140
Db	4110	agtaatcggaagaagcgagacaactctctctgttgggaacgagcagctgtgtgtcatagaag	4169
QY	4141	AGCCCTGCTCCGGCCACTGTAGATTCTCGATTGATTAAGTAAGAACCCACACTGCGCATGGACAC	4200
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QY	4201	AGGACAGAGACTTATTGTATTAAAGAGACATCCGAAAGCAATTTGACAGACTGTACCAATGCT	4260
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QY	4261	GACATTTGCCAATCGGCTGCACACAGGTTTCAAGCTCCGATAGAGATTATGGTGGCGGCCCA	4320
Db	4290	gacattgcccacatcgctcgtacacacagttctcggctctcgaagaatcaatctgtgtcgcca	4349
QY	4321	GGGACAGGTGTGTGGAGTTTGACACCCCATCGTGTCTTGTCTGCCAAGCAGTTCCCGATT	4380
Db	4350	gggacacaggtgtgtggaatttgacaccccatcgctctctctctcaattacagttcaagatt	4409
QY	4381	CTATGCGCATGTTTGGTGTGCTGCACAGAAAGTGTGGCTGTAAAGGCTGACTCCCTCTGT	4440
Db	4410	ctatgcatagtttgcctgcgtcgcaagaacaaggtggtcgttcaaggtcgtgactctccc-gt	4468
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QY	4501	GGCTCTCTCCACGGAACCTGGCTTCCTTCGATTATATCTTGTGGCACAGCATTTCCGGAT	4560
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QY	4561	TGGCTTGCTGTTCACCTTTAGGAGAGTCATATTTTGAATTATGATTAATTCATAT	4620
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QY	4621	TGATGAAACAAATTAATTACTTTTGTGTTCTTAATGTGACATC-TAAAGGTTCAGGGAACG	4679
Db	4642	tcaactaaatgaatctaattccttctgtcttaattgaacttgaagtggttcaggaacca	4701
QY	4680	TTATTTATTAATG-TATCAGAGGCTTAATGAAGCTTATACGTAGCATATATTCATAT	4738
Db	4702	ttactataaatgtatcagtggtgcctataatgaagcttatatgtgtagctatgtcctatat	4761
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RESULT 13
US-60-278-258-6390
: Sequence 6390, Application US/60278258
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
: TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
: TITLE OF INVENTION: Polymorphisms Identified Thereby
: FILE REFERENCE: GX-0010-1 P
: CURRENT APPLICATION NUMBER: US/60/278,258
: CURRENT FILING DATE: 2001-03-23
: NUMBER OF SEQ ID NOS: 17730
: SOFTWARE: PERL Program
: SEQ ID NO 6390
: LENGTH: 4951
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID NO: 1099526.1
US-60-278-258-6390

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Query Match Similarity	76.5%	Score 3710.2	DB 66	Length 4951
Best Local Similarity	97.0%	Pred. No. 0		
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QY	1088	GTTTATATCCTCTTATACCGACGAATGATTTGGATTCACGGCTCCACATATTTTCAGG	1147	
DB	121	gtttatctctcttttaccacagaaatgattttgtcatctcagctcaagcaatttcagag	180	
QY	1148	AGAAATGCGTGGCCGCCACGATGACGTCTCCAGAGATGAATGAATTCTTACTTAC	1207	
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DB	241	attaaattatcaaaatgatgactgcttgcgttcaagaactttctcaggtgttcaagaanaac	300	
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 Db 1201 gaaggaataatgataaagaatacaactctgtgtgacagcgtgcgtgagccgtgag 1260
 QY 2113 CCTGGCAATCTTCCAGACAGCACTGACGAGATTGGAGAGGAGGCAACCTGAG 2172
 Db 1261 cctggccattctctccagcagcgaccttgagcgagattgagagcgaggaagccatctgag 1320
 QY 2173 CGGTGGGACGGCCAGAGAGATCAGCTTGCCGGGCTTGTATATGACAGAGCATCTA 2232
 Db 1321 cgggtggcagcgccagagagatcagccttgcggcgcttgtatagtgacaggaagcatcta 1380
 QY 2233 CATCTTGAGAGACCCCTCAGCTGCTTATGATGCCATGTGGGCAACCATCTTCAATAG 2292
 Db 1381 catcttgagagacccctcagctgacctagatgcccacgttgagcaaccatctccaatag 1440
 QY 2293 TGTATCCGGAACATCTCAAGTCCAAGACAGATTCTGTTTGTATCCACAGTTACATA 2352
 Db 1441 tgcataccggaacatctccaagtcacagacagcttctgtttactccccacagttacagta 1500
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 Db 1801 tgggtctacaatccagcgctgtgggggcccccttgcatctcgtgttattatggcccccttt 1860
 QY 2713 CATGCTAATGTATGACAGACCGGCTTACAGACTGTGTGTTGAGTTACTGTGATCAAGCA 2772
 Db 1861 catgtgaaatgtaagcagcagccttcaagcacttggttgatctgactgataagca 1920
 QY 2773 AGGAAGGGGAAACCACTGTGACTCGAAGAGAGAGACACTCGGTGAGTGCACATGAA 2832
 Db 1921 aggaaggggaaacacacactgactcgaggaagaaagagaccctcgltgagtgacagagaa 1980
 QY 2833 GGACATCTCTATATGACAGTACTATGCCAGCATATACGCCCTCTCATGAGCATGCT 2892
 Db 1981 ggaacatctcataatgactactatgcagacatctaagcccccttccatgagactgact 2040

QY 2893 GATCCTGAAGCCATTGAGAGATGTGCTTTGTCAAGGGCAGGCTGGAGCTTCTCCCG 2952
 Db 2041 gatctgaaagccatctcgagagatgttctgttcaaaaggcagctgagcttccctccg 2100
 QY 2953 GCTGATGACAGAGCTTTTCCGAAGATCCTTCAAGAGCCCTATGAAGTTTGTGACAGAC 3012
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 Db 2461 ctacaataaagggagagaggttctgcacagatatacagagtgctgtgaatgacaaacaaag 2520
 QY 3373 TCTTTTTTTTTTGTATACGTGTGATCGGCTGGCTGGCTGACCTCATAC 3432
 Db 2521 tctttttttttgtgttactagtgatgagtgagtgagtgagtgagtgagtgagtgagtgag 2580
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 QY 3733 CCTCTGCTCTTAAGAAAGTATCTTACGATCAAACTTAAGAGAAAGATTGCAATTGT 3792
 Db 2881 cccctctgtcttaagaagaatctctcaagatacaaaactaaagaagaagatctgcatgt 2940
 QY 3793 GGGGCGGACAGAGATCAGGAAGTCTCGTGGGGATGGCCCTTCTGAGTGGAGATT 3852
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 Db 3001 atctggagcgtcatcaaatatgtatgagtgagataatcagatattggccttgcgacct 3060
 QY 3913 CCGAAGCAACTCTCTATCATTTCTCAAGAGCCGGTGTCTTCACTGACGTGCATGATC 3972
 Db 3061 ccgaagcaaaactctatcatctcctcaagagccggtcgtctgactgagtgagactgacagatc 3120

Query Match	58.6%	Score 2838.6	DB 30	Length 3872
Best Local Similarity	99.8%	Pred. No. 0		
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12	gacgttctaaaggcgacatctgcaatcagtggaacctcgctatgtgcccagcagc	71		
2011	CTGGATCCCTCAATGCTACTGTGAGAGCAACATCTCTTTGGGAGGAATATGATGAGA	2070		
72	ctggatccccaatgctactgcaatcagagaacaatcgttttgggaaggaatagatgaaga	131		
2071	AAGATACAACTCTGTGCTGAACACGCTCTGCTGAGGCTGACCTGGCCATTTCTCCAG	2130		
132	aagatacaacctctgtctgaacagctgtcgtcgtgagccctgacctgcaattctccag	191		
2131	CAGGACCTTGACGAGATTTGAGAGGAGGAGCCACCTGACCGGTGGGAGCGCCAGAG	2190		
192	caggaacctgacgagatgtgagcgagagccaacctgagcgtgtgagcgccagag	251		
2191	GATCAGCCTTCCCGGGCCTTGTATAGTACAGAGAGATCTACATCTGGACACCCCT	2250		
252	gatacagcttgcgggacctgtgataagagagacatcactcctgagacacccct	311		
2251	CAGTGCCTTACATGCCATGATGGGCAACACATTTCAATAGTCTATCCGAAACATCT	2310		
312	cagtgacctgagatgcccatactgtggaacacacatcttaatagtgctatccggaaaaatc	371		
2311	CAAGTCCAGACAGATCTGTTGTTTACCCACACAGTACAGTACCTGTTGACTGTATGA	2370		
372	caagtcgaagcagttctgtttgttaccacacagttacagtlactggttgcgtgatga	431		
2371	AGTATCTTCTTGAAGAAGGCTGTATTATTCGAAAGAGGACACCATATGAGACTGTAA	2430		
432	agtatcttcttgaagaaggctgttattacgaaagagacacatgagaaactgtatga	491		
2431	TTTAAATGAGTACATCTGTCATTTTAAATACCTGCTGAGGAGACACGGCAGT	2490		
492	tttaaatgagatgacatgtctacatctttaaataacctgtgtcgtggaagagacacgcag	551		
2491	TGAGATCAATTCANAAAAAGAAACAGTGGTTCACAGAAAGATTCACAGACAAAGGCTC	2550		
552	tgagatcaattcaaaaaagaaaccagtggttcaagaaagttcaacaagacaaggtcc	611		
2551	TAAACAGGATCAATTAAGAAGCAAAAAAGCAGTAAGCCAGAGAAAGGCGAGCTTGCA	2610		
612	taaaacagagatcagtaaaagaagaaaaagcagtaaaagccagaggaagcgactgtgca	671		
2611	GCTGAGAGAGAAAGGAGGAGGCTCAGGCGCTGCTGATATGATGAGTCTACATCCAGC	2670		
672	gctggaagagaaaaggaaggttcaagtgccctgtgtcaatatacgtgttcaacatccagc	731		
2671	TGCTGGGGGCGCCTTGGCATTTCTGGTATTAATATGGCCATTTTCATCTGATATGAGCAG	2730		
732	tgctgggggccccttgcatctcgtgtatatacggccctttaaigtgaagttagcag	791		
2731	CACGCGCTTACGACACTGCTGGTGTGAGTTACTGTGATCAGAACAGAAAGCGGGAACACAC	2790		
792	cacgcgcttaagcaacctgtgtgtgtgtactgtatcaagcaaggaagcggaacaccac	851		
2791	TGTGACTCGAGGGAGACGACGCTCGGTGATGACAGATGAGAACAAATTCCTATATGCA	2850		
852	tgtgactcgaggaagacgacctcgtgtgagtgacagcatgaagaacaatcctatactga	911		
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OY 2911 AGGAGTGTCTGTGTCAAGGGCAACGCGAGAGCTTCTCCGGGTGATGACGAGCTTTT 2970
Db 972 agagatgtctctgtcaagagcagctgacgagctcctccgcgtgacgagcgtctt 1031
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Db 1152 gtccatccagaacgtatccctgtctctgtctgtgagagatgacgagagctctccc 1211
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Db 1212 gtgtgtcctgtgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1271
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Db 1332 ccacatcagctccagacataagagctctgacacacacacacacacacacacacacac 1391
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Db 1392 gtctctgacagatcacagagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1451
OY 3391 GTGTGCGATGCGGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 3450
Db 1452 gt 1511
OY 3451 CAGGGGCTGATGATGCTGTGATGACGGGAGATTCCTCCAGGCTATGGGGTCTGCG 3510
Db 1512 caagggctgt 1571
OY 3511 CATCTCTTATGCTGTCCAGTTAAAGGGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 3570
Db 1572 catctctatgtctgtcaagtgatgaagtgatgaagtgatgaagtgatgaagtgatga 1631
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Db 1632 gacagagctgt 1691
OY 3631 GGAAGACCTGCGCAAGATTAAAGAACAGGCTCCCTCCCTGACGTGGCCCGGAGGAGA 3690
Db 1692 ggaagacctgcgcaagattaaagaaagagctccctccctgtgtgtgtgtgtgtgtgt 1751
OY 3691 GGTGACCTTTGAGAACGACAGATGATGATGATGATGATGATGATGATGATGATGAT 3750
Db 1752 ggtgacctttgagaagcagaatgagtgatcaggaagaaacccctctctgtgtgtgt 1811
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Db 1872 gaagtgctcgt 1931
OY 3871 GATTGATGAGTGAATCAAGTATGATGATGATGATGATGATGATGATGATGATGAT 3930
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OY 3931 CATTCCTCAAGAGCGGT 3990
Db 1992 cattcctcaagagcggt 2051

OY 3991 CCAGTACACTGAAGACAGATTTTGGATGCCCTGAGAGACACACATGAAGAATGTAT 4050
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OY 4111 GGGGGAACGGCAGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4170
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Db 2471 ggt 2530
OY 4471 CATTCCTGCTGGGGGCGGGCCCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4530
Db 2531 catctccctgt 2589
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OY 4591 CATATTTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4650
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Db 2770 agcttataagtgtagctataatcatalataatcctgtgaacacccatatttccagtg 2829
OY 4771 AAATGTAAGCTGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4830
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Search completed: August 11, 2002, 11:01:58
Job time: 6288 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 09:18:35 ; Search time 627.48 Seconds
(without alignments)
18845.237 Million cell updates/sec

Title: US-09-528-031-1
Perfect score: 4847
Sequence: 1 GGCCTCAGCTCGGAGCGCTG.....AAAAAAAAAGGCGCCGC 4847

Scoring table: IDENTITY: NUC
Gapop 10.0 , Gapext 1.0

Searched: 1437365 seqs, 1219827628 residues

Total number of hits satisfying chosen parameters: 2874730

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4792.6	98.9	5838	US-09-647-140A-3	Sequence 3, Appl1
2	4792.6	98.9	5838	US-10-007-925A-325	Sequence 325, App
3	4307.6	88.9	4314	US-10-154-452-1	Sequence 1, Appl1
4	3929	81.1	3978	US-10-154-452-5	Sequence 5, Appl1
5	3142	64.8	5881	US-10-172-086-81	Sequence 81, Appl1
6	3011	62.1	5881	US-10-172-086-82	Sequence 82, Appl1
7	768	15.8	4862	US-10-087-782A-1	Sequence 1, Appl1
8	725.4	15.0	4083	US-10-162-012-35	Sequence 35, Appl1
9	725.4	15.0	4638	US-10-162-012-33	Sequence 33, Appl1
10	591.8	12.2	1579	US-10-137-337-228	Sequence 228, App
11	511.2	10.5	5011	PCT-US02-07787-35	Sequence 35, Appl1
12	511.2	10.5	5011	US-09-442-384B-504	Sequence 504, App
13	437.4	9.0	4231	US-09-930-213-287	Sequence 287, App
14	437.4	9.0	4231	US-09-647-140A-1	Sequence 1, Appl1
15	409.8	8.5	426	US-10-011-154-3846	Sequence 3846, App
16	401.4	8.3	457	US-09-918-995-28384	Sequence 28384, A
17	376.8	7.8	5099	US-10-191-803-60	Sequence 60, Appl1
18	363.6	7.5	4977	PCT-US02-18947-472	Sequence 472, App
19	363.6	7.5	4977	US-10-172-118-472	Sequence 472, App
20	362.4	7.5	4509	US-09-647-140A-7	Sequence 7, Appl1
21	356	7.3	5079	US-09-647-140A-5	Sequence 5, Appl1
22	351.6	7.3	6628	US-10-191-803-61	Sequence 61, Appl1
23	349.2	7.2	4869	US-09-935-625-26954	Sequence 26954, A
24	344.4	7.1	4869	US-09-935-625-26571	Sequence 26571, A
25	340.8	7.0	4896	US-09-935-625-3325	Sequence 3325, Ap

26	340.8	7.0	4896	US-09-935-625-26040	Sequence 26040, A
27	334.6	6.9	4872	US-09-935-625-3010	Sequence 3010, Ap
28	334.6	6.9	4872	US-09-935-625-25376	Sequence 25376, A
29	306.4	6.3	1981	US-09-919-002-2634	Sequence 2634, Ap
30	301.2	6.2	489	US-10-007-926A-324	Sequence 324, App
31	300.8	6.2	4551	US-09-935-625-5375	Sequence 5375, Ap
32	300.8	6.2	4551	US-09-935-625-8195	Sequence 8195, Ap
33	300.8	6.2	4551	US-09-935-625-20408	Sequence 20408, A
34	300.8	6.2	4551	US-09-935-625-25429	Sequence 25429, A
35	289.8	6.0	1110	US-10-198-717-7	Sequence 7, Appl1
36	288.8	6.0	1098	US-10-198-717-4	Sequence 4, Appl1
37	278.4	5.7	4369	US-09-935-625-7276	Sequence 7276, Ap
38	278.4	5.7	4369	US-09-935-625-16232	Sequence 16232, A
39	251.2	5.2	4566	US-09-935-625-5575	Sequence 5575, Ap
40	251.2	5.2	4566	US-09-935-625-8786	Sequence 8786, Ap
41	251.2	5.2	4566	US-09-935-625-21006	Sequence 21006, A
42	251.2	5.2	4566	US-09-935-625-25853	Sequence 25853, A
43	248	5.1	4548	US-60-360-039-25324	Sequence 25324, A
44	246.4	5.1	4524	US-60-360-039-27791	Sequence 27791, A
45	232.8	4.8	4338	US-60-360-039-25928	Sequence 25928, A

ALIGNMENTS

RESULT 1	US-09-647-140A-3	Sequence 3, Application US/09647140A	
GENERAL INFORMATION:			
APPLICANT:	Fox Chase Cancer Center		
APPLICANT:	Kruh, Gary D.		
APPLICANT:	Lee, Kun		
APPLICANT:	Belinsky, Martin G.		
APPLICANT:	Bain, Lisa J.		
TITLE OF INVENTION:	MRP-Related ABC Transporter Encoding		
FILE REFERENCE:	Nucleic Acids and Methods of Use Thereof		
FILE REFERENCE:	FCCC 98-02		
CURRENT APPLICATION NUMBER:	US/09/647,140A		
CURRENT FILING DATE:	2001-05-21		
PRIOR APPLICATION NUMBER:	PCT/US99/06644		
PRIOR FILING DATE:	1999-03-26		
PRIOR APPLICATION NUMBER:	60/079,759		
PRIOR FILING DATE:	1998-03-27		
PRIOR APPLICATION NUMBER:	60/095,153		
PRIOR FILING DATE:	1998-08-03		
NUMBER OF SEQ ID NOS:	18		
SOFTWARE:	FastSeq for Windows Version 3.0		
SEQ ID NO 3			
LENGTH:	5838		
TYPE:	DNA		
ORGANISM:	Homo sapiens		
US-09-647-140A-3			
Query Match	98.9%	Score 4792.6;	DB 5; Length 5838;
Best Local Similarity	99.8%	Pred. No. 0;	
Matches 4809;	Conservative	0; Mismatches	9; Indels 1; Gaps 1;
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11	ggctcatgctcggagagtggttgagcgcgctgcttgtagcagggcgag	70	
61	GAATTCGATGTGAACATCAACAGCTGTGAGCCTCGAACCTCAGACAGAAATGAA	120	
71	gaattcgaatgtgaacatcaacagctgtgagcctcgtaacctcagagagaatgaa	130	
121	GGATATGACATAGAGAAAGATATATCATCCAGTCCGTGATGAAATGAGAGGA	180	
131	ggatatagacataagaaagatataatccaccagctccggatagaagtgtgagagga	190	
181	GAGAACGACACTTCTGGGAGCAGACAGACCGTGAAGATTCAAGTTACAGAGAACTCG	240	
191	gagaaacgacctcttggaagcagagacccgtaagattccaagtgcagagaaactcg	250	

OY	241	ACGTTGGAAATGCCAAGATGCCCTTGGAAACAGACAGCCGACCGGAGGCGCTCTCTTTGA	300
Db	251		
OY	301	AGCGTTGAAATGCAATTCAGCTCAGAAATCCCTGAGATGAGACATCTCCAGGAAGAAATACA	360
Db	311	tgctccatgatctctcagctcagaaatccctgatatgtagagagacatcccaaggaaagtaccca	370
OY	361	TCATGCGTTGAGTGTCTGAAAGCCCATCCGACTACTTGTGCAAAACACAGACCCAGCTGGA	420
Db	371	tcattgcttagtgcctcgaagcccatccgagactacttccaacaacacagaccagtgga	430
OY	421	CAATCTGGGGCTTTTTCCTGTATGACTTTTGGTGGCTTCTTCTCTGCGCCGTGTGC	480
Db	431	caatgcgtggtcttttccctcgtatgaacttttcgttgcttctctccctcgtcccggtgtgc	490
OY	481	CCACAGAAGAGGGGAGCTCTCATATGGAAGAGTGTGGTCTCTGTCCAAACAGAGCTTC	540
Db	491	ccacaagaagg999ggtcctcaatggaagagcgtgtgtctctgtccaagcaagatcttc	550
OY	541	TCAGCTGAACGCGAAGACACACAGACACACCTGTGGCAAGAGCTATGAAAGTTGGCC	600
Db	551		
OY	601	ACAGCTGCTTCCCTGGCGAAAGGTTGTGTGATCTTCTGCGACACAGAGCTATCTGTC	660
Db	611	agaagctgctccctcgtcgaaggtgtgtgtatctctcgtccagcaagctcatctgtc	670
OY	661	CATGCTGGGCTGATGATCACAGCAGCTGCGCTTACATGAGACAGCCTTATGATGA	720
Db	671	catcgtgtgcttgatgatacaagcagctcgtgtgcttcaatgtgacccgctcatagttaa	730
OY	721	ACACCTCTTGGAGATACCCAGCGAACAGAGTCTTAACCTGACAGTACAGTTGTGTAGT	780
Db	731	aaacctcttgagatatacccaagcaaaagtgcttaacctgcagtaagcttgttgcgt	790
OY	781	GCTGGGCTCCTCTGACGGAAATCGTGGGCTTGTGTCGTTGCATGACTTGGGCAAT	840
Db	791	gctggcctctctctcgtacggaatcgtgcgtcttgctgctgtcacgtactgtgcatt	850
OY	841	GAATATCCGAAACCGGTGCGGCTTGGCGGGGGGCATCTAACCATGAGGCTTAAACAAT	900
Db	851	gaattaccgaacccggtgtccgcttgcgg9999gccaaccataacatggtcattlaagaat	910
OY	901	CCTTAATTTAAAGAACTTAAAGAAATCCCTGGGTGAGCTCATCAACTTGTCTCAA	960
Db	911	ccctaagttaaagaacattaaagaatccctgggttgagctcatcaaatctgtccaa	970
OY	961	CGATGGGAGAGATGTTTGAAGCAGACGCGGTGGACCCGTGCGTGGAGAGACCCGT	1020
Db	971	cgaatggcagaagaatgcttgaagcagaacgcgtctggcagccgtgcgtgtgagagccgct	1030
OY	1021	TTGTTGCCATCTTAGCATGTATTTATATGATTAATTAATTCGTGGACCAACAGGCTTCTGG	1080
Db	1031	tgttgcactcttagcattgattataatgaaatattctcgtggacaacaagcgttccgtg	1090
OY	1081	ATCAGCTGTTTTTATCCTCTTTTACCAGCATGATGTTTGCATCAGCGCTCACAGATA	1140
Db	1091	atcagctgttttattctctctttaccacaagaatgattgttcatcaacggtccaacagata	1150
OY	1141	TTTACAGAGAAATGCTGTGCGCCGACAGGTGAACGTGCGCAAGAGATGATGAAAGTTCT	1200
Db	1151	tttcaggaagaatgctgtgcgcgcacggaatgaaacgtgtgccagaagaatgaagtctt	1210
OY	1201	TACTTACATTTAAATTTATCAAAATGTTATGCTGTGGCTCAAAAGCATTTTCTCAGAGTTTCA	1260
Db	1211	tacttacaattaaattatcaaaatgtaatcgtcgtgtcaagaattttctcagagtgttca	1270
OY	1261	GAATAATCCGGAGAGAGAGAGTGGATATTGGAAAAAGCCGSGTACTTCCAGACATCAC	1320
Db	1271	aaaaatccgagagagagagctgcgatacttgaaaaagccggtatcttccagaggtatcac	1330

QY	1321	TTGGGGTGTGGGTCCCATTTGGTGGGTGATGTTCCAGCGTGTGACTCTTCTGTTCATAT	1380
Db	1331	TGtgggtgtgtgtcccatcttgcgtgtgactgtccagcgtgtgtbaacctctcgttcacat	1390
QY	1381	GACCGTGGGCTTCGATCTGACAGACGACAGGGCTTTCACAGTGTGACGTTCATATTC	1440
Db	1391	gaacctgggtcttgatctcgtgaacgaagacacaggtcttcaacgtgtgtgaacgtcttcaatlc	1450
QY	1441	CATGACCTTTGGCTTGAAGTTACACCGTTTTCAGTAAAGTCCCTCTCAGAAAGCTTCAGT	1500
Db	1451	catgaccttgccttgtaagaatcaacccgttttcagttaaagtcctctcgaagcctcagt	1510
QY	1501	GGCTGTGACAGATTTTAAAGATTTGTTCTTCTTAATGGAAGAGGTTCCACATGATTAAGACAA	1560
Db	1511	ggctgttbaacagatttaagagtltgttcttaagtgaagagtgttcacatgataaagaaca	1570
QY	1561	ACCAGCCAGTCCATCATCAAGATAGAGATGAAGAAATGACACTTGGCATGGGATCCCTC	1620
Db	1571	accagccagttcctcaatcaagaatagaagaatgaaaaatgcacctgtgcgtgtgactcttc	1630
QY	1621	CCACTCCAGTATCCAGAACTGGCCCAAGCTGACCCCAAAATGAAGAAAAGACAAAGAGGC	1680
Db	1631	ccactccagtatccagactgtcccaagtgcacctccccaatgtaaaaagataaagatgagc	1690
QY	1681	TTTCCAGGGGCAAGAAAGAAAGGTGTGAAGCACTGTCAAGCGCACTGACATCAGCGGTCT	1740
Db	1691	ttccagtggtgcaagaagaagaagtgtgaagcagctgtgcagcactgtgactcaagtcggtct	1750
QY	1741	GGCAGAGAGAAAGGCAACCTCCCTCGGACATGTACGAGGCGCCACGACCCGAAGAGGA	1800
Db	1751	ggcagagagagaagaagccaactctctctgtgaacagtgtgcagtcgagccagtcctcggaagga	1810
QY	1801	AGAAAGCAAGACATTCACCTGGGCCCACCTGTCCCTTACAGAGACACTGCACAGCATCGA	1860
Db	1811	agaagtgcaagacatccacactgtggccaactgtcgtcttaagaggtacactgtcaagatctga	1870
QY	1861	TCTGAGATGCCAAGAGGTAACTGGTGTGAATCTCGCGCACTGTGGGAATGCGAAAAC	1920
Db	1871	tctgtagatcccaagaaggttaactggtgtgaaactgtcgtgcagctgtgtggaagtgtgaaaaac	1930
QY	1921	CTCTCTCATTTCCAGCAATTTTAGGCGCAGATGACGGCTTTCAGAGGGCAGCATTTGGCAATCAG	1980
Db	1931	ctctctcaatttcagccatttaggtccaagatgaacgctcttcagaaggtgcacatgtcaatcag	1990
QY	1981	TGGAACCTTCGCTTATGTGTGGCCAGCAGAGGCTGTGATCTCAATGTCTACTGTAGAGACAA	2040
Db	1991	tggaaactctgtattgtgtgccagaagcgcgtgactcctcaatgtactctcgtgagagaca	2050
QY	2041	CATCTCTTTTGGGAAGAAATATATGATAAAGAAATATCAACTGTGTCTGAAACAGCTGCTG	2100
Db	2051	catctctgttttgggaagaatatagtatgaagaagaatacaactctgtgtcgtgaacagctgtctg	2110
QY	2101	CCTGAGCGCTGACCTGGCCATTTCTTCCAGACGACGACCTGACGGAGATTTGGAGGCGGAGG	2160
Db	2111	cttgaagcctggaactgtgcacattcttcccaagcagcagcctgtgaagatcttgaagagcgag	2170
QY	2161	AGCCAACCTGAGCGGTGGGACGCGCCAGCAGAGATATCAAGCTTGGCCCGGCTTGTATATGA	2220
Db	2171	agccaacctgagcggtgtgagcggtccaagagatcaagcttgccttgctgattagtga	2230
QY	2221	CAGAGACATTAATCTGTGAGACACCCCTCTAGTGTGCTTACATGCCCCATGTGGCAACCA	2280
Db	2231	cagagacattacatctctgtgaacgacccctcagtgctttagatgcccattgtgtgtgcaacca	2290
QY	2281	CATCTTCAATAGTGCATCCGGAACATCTCAAGTCCAAAGACAGTCTGTTTGTATACCA	2340
Db	2291	catcttcaatagtgcatctccggaacaatcctcaagctcaagacattcgtttgtttaccca	2350
QY	2341	CCAGTTTACAGTACTGTTGTGATCTGATATCAATGATCTTCAATGGAAGAGGCGTGTATTAC	2400
Db	2351	ccagttacagtactgtgtgtacgtgtgaagaagtgtcttctctatgaagaagaggtcgttatctac	2410
QY	2401	GGAAAGAGCACCATAGAGAACTGATGAATTTAAATGATGATCATCTACCATTTTATA	2460

Db 2411 ggaagagggaccacataggaacatgaaattaaatgagctatctacattttaa 2470
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Db 2471 taacctgtgctggagagacaccgcagcttgagatcaattcaaaaagaacagctgg 2520
OY 2521 TTACAGAAAGAGTCAACAAACAAAGGCTCTAAACAGATCATTAAGAAGAAAGC 2580
Db 2531 ttcaagaaagatcaacaagaagagctcctaaacagatcagtaagaagaaaaagc 2520
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Db 2651 ctggtcagatatagtgtgtctacatccagctgtgaggggcccttgcatctcgttat 2710
OY 2701 TATGGCCCTTTTCAATGCTGAATGTAGACACCGCCTTACAGCACTGGGTGAGTTA 2760
Db 2711 taagccctctcaatgctgtaagttaagagcaaccgcttcaagcaccggtgtgtatga 2770
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Db 3011 ttgtgaacagacccccaaggaagatcttcaacaggtttccaaaacatgagtagt 3070
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QY 4621 TCATGTAAACAAATTTAGCTTTTGTCTTAATTCACCTCTAAAGGTTACAGGAAACCGT 4680
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Db 4810 aagcactgtgctaataca 4828

RESULT 2
US-10-007-926A-325
Sequence 325, Application US/10007926A
GENERAL INFORMATION:
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: HOUIGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: FERRI, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007, 926A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254, 090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 325
LENGTH: 5838
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES: atp-binding cassette, sub-family c
OTHER INFORMATION: (citr/mrp), member 5 (ABCC5) gene.
US-10-007-926A-325

Query Match 98.9%; Score 4792.6; DB 7; Length 5838;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4809; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 GGCATGCTCTGGGAGCGGTGTGAGCGGCGGCTTGTCTTGAGACAGGCGCGAC 60
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Db 11 ggcataagctcggagagcgtgtgagcgctgctgctgagcgagcgagcgagcgag 70
QY 61 GAATTCGTATGTAAGTAAGTGTGAGCGCTGTAACCTCCACTAGAGAAATGAA 120
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Db 71 gaattctgattgtaaacatacagctgtgagcctcggaacctcgctcagaagaatgaa 130
QY 121 GGATATGACATAGGAAAGATATATCATCCAGTCCTGGGTATAGAAAGTGTAGGA 180
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Db 131 ggaatacagataagaaagagatatcatcccgctcctggtatagaaagtgtgagga 190
QY 181 GAGAACACGACTTCTGGGAGGACAGAGACCGTGAAGATTCCAAAGTTCCAGAGAACTCG 240
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Db 191 gagaacacagcattctgagacgacagacgacgacgacgacgacgacgacgacgac 250
QY 241 ACCGTGGAATGACAGATGCTTGAAGACAGAGCCGAGCCGAGGCGCTCTCTCTGA 300
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Db 251 accgttggaatgacagatgcttgaagacagacgacgacgacgacgacgacgacgac 310
QY 301 TGCTTCATGATCTTCTAGCTCAGATCTTGATGAGAGAGATCCCAAGGAAAGTACCA 360
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QY 361 TCATGCTGTAGTGTCTGAGAGCCCATCCGAGACTTGTGAAACACACAGACCACTGGA 420
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QY 481 CCAGAAAGAGGAGAGCTCTCAATGGAAGAGCTGTGCTCTGTGCAAGACAGACTTTC 540
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RESULT      3
US-10-154-452-1
; Sequence 1, Application US/10154452
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Roy, Josee
; APPLICANT: Connop, Bruce P.
; TITLE OF INVENTION: INCREASED FUNCTIONAL ACTIVITY AND/OR
; TITLE OF INVENTION: EXPRESSION OF ABC TRANSPORTERS PROTECTS AGAINST THE LOSS OF
; FILE REFERENCE: 100103.420
; CURRENT APPLICATION NUMBER: US/10/154,452
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-154-452-1

Query Match      88.9%; Score 4307.6; DB 7; Length 4314;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4310; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Q 3896 ATTGGCTTGGCGACCTCCGAGCAAACTCTTATCAATTCCTCAAGAGCCGGTCTGTT 3955
D 3781 attggtcttgcgagcctccgaaagaaactctatcatcttccaaagccggtgctgtc 3840

Q 3956 AGTGGCATGTGTGATCAATTAATTTGACCCCTTACACAGTACATGAAGACAGATTGG 4015
D 3841 agtggcatgtgtgacatcaaatcttgagaccccttcaacagatacactgaagaccagattgg 3900
Q 4016 GATGGCCCTGGAGAGGACACACATGAAGAATGATTGCTCAGCTTACTCTGAAACTTGA 4075
D 3901 gatggccctggagagacacacatgaagaatgattgtctcagcttactcctgaacttgaa 3960
Q 4076 TCTGAATGATGAGAAATGGGATTAATCTCTGAGTGGGGAAGCGAGCTCTTGTGAT 4135
D 3961 tctgaatgatagagataagataaactctcagtgagggaacagagatcttgatgata 4020
Q 4136 GCTAAGACCTCTGCTCCGACCTGTAAATTTGATTTAGATGAAGCCACACCTGCAT 4195
D 4021 gctaaagccctgctccgcacactgaagatcttgattagatgaagccacagctgcatg 4080
Q 4196 GACACAGACAGACTTATGATTTCAAGAGACCATCCGAGAGCATTTCACACTGTACC 4255
D 4081 gacacagacagacttattgattcaagagacatccgaagacatttgacagctgtacc 4140
Q 4256 ATGCTGACCATTTGCCATGCGCTGCACAGGTTTCTAGCTCCGATGATTAAGTGTGCTG 4315
D 4141 atgctgacattgcccactgcctgcacagtgctcagagctccgataagatattgtgtcgtg 4200
Q 4316 GCCCAGGACAGGTGTGAGTTTGACACCCCATCGGTCTTCTGTCCACAGCAGTTTC 4375
D 4201 gcccaaggacaggtgtgtgagtttgacacccacatcgctcctctctgtccaaagacgttcc 4260
Q 4376 CGATTCTATGCCATGTTGCTGCTGCAGAGAACAGTGTGCTGAAGGGCTGA 4429
D 4261 cgattctatgccatgttgcctgctgcagagaaaggtcgtcgtcaagggtcga 4314

RESULT 4
US-10-154-452-5
Sequence 5, Application US/10154452
GENERAL INFORMATION:
APPLICANT: Relner, Peter B.
APPLICANT: Roy, Josee
APPLICANT: Conop, Bruce P.
TITLE OF INVENTION: INCREASED FUNCTIONAL ACTIVITY AND/OR
TITLE OF INVENTION: EXPRESSION OF ABC TRANSPORTERS PROTECTS AGAINST THE LOSS OF
TITLE OF INVENTION: DOPAMINE NEURONS ASSOCIATED WITH PARKINSON'S DISEASE
FILE REFERENCE: 100103.420
CURRENT APPLICATION NUMBER: US/10154.452
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 3978
TYPE: DNA
ORGANISM: Homo sapiens
US-10-154-452-5

Query Match 81.1%; Score 3929; DB 7; Length 3978;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 3932; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Q 116 ATGAAGATATCGACATATGAAAGAGATATATCATCCCACTCCGCTGATTAAGATGTG 175
D 1 atgagagatatacgacataagaaagatatacatcccaactcctggtatagaagtgtg 60
Q 176 AGGAGAGAACACGACCTTCTGAGCAGACAGACCTGTAAGATTCCAAGTTCAAGAGAGA 235
D 61 aggagagaaacacgactctctgagcagacagagacgttgatgaattccaagtcaagaga 120
Q 236 ACTGACCGTTGGAATGCCAAAGATGCTTGAACACGACGCCGAGCGGAGGCTCTCT 295
D 121 actgaccggttggaatgccaagatgcttgaacacgacgccgagccgagggcctctct 180
Q 296 CTGATGCTTCATGATCTTCTCAGCTCAGATCTGATGATGAGGACATCCCAAGGAAAG 355

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Db 181 ctgatgctccacatcctcagctccagatccgtagtggagcatcccaaggaaag 240
OY 356 TACATCATGGCTTGAGTGCCTCTGAAGCCATCCGGAGTACTTGGAACACACGACCCA 415
Db 241 TACATCATGGCTTGAGTGCCTCTGAAGCCATCCGGAGTACTTGGAACACACGACCCA 300
OY 416 GTGACAAATGCTGGCTTTTTCCTGATGACTTTTTCGCTGCTTCTCTGAGCCGT 475
Db 301 gtggacaatgtcgtcttttctctgtatgacttttctgtcgtcttctctctgcccgt 360
OY 476 GTGACCCCAAGAAAGGGGAGCTCTCAATGGAAGAGCTGTGGTCTGTGTCCAGCAG 535
Db 361 gtggcccaagaagggagctctcaatggaagacgtgtgtctgtctccagaagag 420
OY 536 TCTTCTGACGTGAATCGAGAAAGACTAGAGACTGTGGCAAGAGACTGAATGAAT 595
Db 421 tctcttgcgtgaaactcgaagaactagaagactgtgtgcaagaagagctgaatga 480
OY 596 GGGCAGACGCTGCTCCCTCGAAGGGTGTGTGATCTTCTGCGCAGCAGGCTCATC 655
Db 481 gggccagaagctgtctccctcgtgaaaggtgtgtgtatctctcgtccgacaggtc 540
OY 656 CTGTCACTCGTGTGCTGATGATCAGCAGCTGTGCTTCACTGAGCAGCAGCTTCATG 715
Db 541 ctgtccatcgtgtcgtatgatacagcagctgtcgtctcagtgagcagccctcatg 600
OY 716 GTGAAACACTCTTGAGATATACCAAGCAACAGACTTAACTGACTACAGCTTGTG 775
Db 601 gtgaaacacctcttgagatacaccagcaacagagctaaccttgcagtaacagctgt 660
OY 776 TTATGCGGGCTGCTCCCTGAGGAAATCGTGGGCTGTGCTGCTGCACTGACTGG 835
Db 661 ttatgtcggggccctccctcgtgaaacgtgtcgtgtcgtgtcgtcgtcgtcgtcgt 720
OY 836 GCATGTGATATCCGACACGGTGTGCTGCTGCGGGGCACTTAACTGAGCAATTTAG 895
Db 721 gcatgtaatcagcaacccgtgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 780
OY 896 AAGATCTTAAATTAAGACATTAAGAAATCCCTGGGTGAGCTCATCAACTTTGC 955
Db 781 aagatcttaagttaagaacattaaagaatccctgggtgtgagctcatcaacttgc 840
OY 956 TCGAAGCATGGGAGAGATTTTGAGGACAGACGCTTGGCAGGCTCTGGCTGAGAG 1015
Db 841 tcccaagatggcagaaatgttctgagcgacgacgctgtgacgctgtgtgtgagaa 900
OY 1016 CCCGTTGTGCACTTGAAGCATGATTAATGATTAATTTTGGGACCAAGGCTTC 1075
Db 901 cccgtgtgtcgaatcctgagcaatattatataatattcctgtggacaaacagcttc 960
OY 1076 CTGGGATCAGCTGTTTATCTTATCCAGCAATGATGTTGATCAAGGCTCA 1135
Db 961 ctgggatacagctgttttatctcttaccacagcaatgattgttgatcaacgctaca 1020
OY 1136 GCATATTTACAGAGAAAATCGGTGGCCGACAGATGAAGCTGTCCAGAGATGAATA 1195
Db 1021 gcatattcagagaaatgtgtgtcgcgcagatgagacgtgttcagaaagatgaat 1080
OY 1196 GTTCTTACTTCAATTAATTAATCAAAATGATATGCTGGGCAAGCAATTTTTCAGAGT 1255
Db 1081 gtcttactcaatlaaattatcaaaatgtatcctgtgtgtgtgtgtgtgtgtgtgt 1140
OY 1256 GTTCAGAAAATCCGAGAGAGAGCTGTGATATTGGAAGAACCGGGTACTTCCAGAGC 1315
Db 1141 gtccagaaaatccgagagagagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200
OY 1316 ATCACTGTGGGTGTGCTCCCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1375
Db 1201 atccctgt 1260
OY 1376 CATATGACCCCTGGGCTTGATCTGACACAGCAGGCTTACAGTGTGTGACAGTCTTC 1435
|||||

Db 1261 cataagaccctgtgtcgtatcgtacagcagcacagcttccacagtggtgtacgtcttc 1320
OY 1436 AATTCATGACTTTTGTGAAAGTAACACCGTTTGTAGTAAGTCCCTCCACAGAC 1495
Db 1321 aatccatgacttctgtctgtgaaagtaaacacgcttctcaagtaaaatccctccaaagc 1380
OY 1496 TCACTGCTGTGTGACAGATTAAGATTTGTTTCTTAATGGAAGAGTTTACATGATTAAG 1555
Db 1381 tcaagt 1440
OY 1556 AACAAACCAAGCAGCTCTCAATCAATGATGATGATGAAATGCACTTGGCATGAGAC 1615
Db 1441 aacaacacagcagctccatcaatcaagatagatgaaatgtgcaacctgtgcatggag 1500
OY 1616 TCCCTCCACTCCAGATACAGACTCGCCCAAGCTGACGCCCAAAATGAAAAATCACAG 1675
Db 1501 tctcccaatccagatccaaatcgcgcgaagctgtaccccccaaaatgaaaaagacaag 1560
OY 1676 AGGCTTCCAGGGGCAAGAAAGAGAGAGTGAAGGCTGACGCGCACTGAGCATGAGCG 1735
Db 1561 aggtcttccaggggcaagaagaagaaggtgtgagcagctgtcagcgtacgtacatcagc 1620
OY 1736 GTGCTGAGAGCAGAAAGGCCACCTCTCTGACAGTGAAGAGAGGCGCCACAGTCCGAA 1795
Db 1621 gtgtcgtgagagcagaagaagccacctctcctgtgacagtgagcagcgtcccgaa 1680
OY 1796 GAGGAAGAAGCAGACATCTCAGCTGGGCCACCTGCGCTTACAGAGACACTGCACAGC 1855
Db 1681 gaggaagaaggaacacatccacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1740
OY 1856 ATCGATCTGAGATCCAGAGAGAGGTAACTGTGTGAATCTCGGAGTGTGGAAAGTGA 1915
Db 1741 atcgatcgtgagatccaaagaaggttaactgtgtgtgtgtgtgtgtgtgtgtgtgt 1800
OY 1916 AAAACCTCTCTATTTCAGCCATTTTAGCCAGATGACGCTTCTAGAGGCAAGATTGCA 1975
Db 1801 aaacctctccatctttagcattttagccagatgacgtcttctagaggagcaatgca 1860
OY 1976 ATCACTGGAACCTTGGCTTATGTGTGCGCCAGCAGGCTGTGATCTTAATGCTTGTGA 2035
Db 1861 atcagtggaacctgt 1920
OY 2036 GACAAACATCTGTTTGGAGAGAAATGATGAAAGAAATCAACTGTGTGTGAACAGC 2095
Db 1921 gacaaatccctgt 1980
OY 2096 TGTGCTGAGAGGCTGACCTGGCCATCTTCTCCACAGCAGCACTGACGAGATTGAGAG 2155
Db 1981 tgtgtcctgagagcctgtgacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2040
OY 2156 CGAGAGCCAACTGAGCGGTGGGACGCCAGAGATCAGCTTGTGCCGGGCTTGTAT 2215
Db 2041 cgaagagcaacctgt 2100
OY 2216 AGTGACAGAGACTATATCTGTGACGACCCCTCATAGTGTGATGATGCCATGTGGGC 2275
Db 2101 agtgacaggaagatctatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2160
OY 2276 AACCATCTTCAATAGTGTATCCGGAACATCTCAAGTCCCAAGAGCTTCTGTTTGT 2335
Db 2161 aaccacatcttcaatagtgatcctcggaaacatctcaagtlccaagaacgttctgtttgt 2220
OY 2336 ACCCAGAGTTACAGTACCTGGTTGACTGTGATGAATGATGATGATGATGATGATGAT 2395
Db 2221 aaccacagttacagttacgt 2280
OY 2396 ATTACGGAAGAGCAGCCATGAGAGACTGATGAATTTAAATGGGACTATGCTACAT 2455
Db 2281 attacggaagaagagacccaatgaagaaatgtatgaaatgtgtgtgtgtgtgtgtgt 2340
OY 2456 TTTAATAACCTGTTGCTGGAGAGACACCGCAGTTGAGATCAATTTAAAAAGAAAC 2515
Db 2341 ttataaacctgt 2400

OY	2516	AGTGGTTACACGAAGAAGTCAACAAGACAGAGGCTCTTAAACAGATCAATTAAGAAGAA	2575
Db	2401	agtgggttcacagaagaagatcacaagaacaagggctccaaacaagatcagtaagaagaa	2460
OY	2576	AAAGACGTAAGAAGCCAGAGGAAAGGGCAGCTTGTGTACACTGTGAAGAGAAAGGGACGGCTTCA	2635
Db	2461	aaagcagttaagagccagaaggaagggcagcttggcagcttggaaagaadaaggggacaggttca	2520
OY	2636	GTGGCCGTGTGACATATATGGTGTCTACATCCAGAGCTGCTGGGGGGCCCTTGGCATTCCTG	2695
Db	2521	gtgcgccgtgtacagatatagttgcctaataccagcgtcgtcgggggccccttggatctctg	2580
OY	2656	GTTATATGAGCCCTTTTCATAGCTGTAATGTAGCAGCAGCCGCTTAGAGCACTGTGTGTTG	2755
Db	2581	gttatatagcccttcttcacgtcgtgaatgttaggaagaccgcttcagcaacctgtgtgtg	2640
OY	2756	AGTTACGTGAATCAAGCAAGGAAGCGGGAACACACTGTGTACTTCGAGGGGAAGAGACCTCG	2815
Db	2641	agttacgtgatacaagcaaggaagcgggaacaacacactgtgtactcgggggaacagagacctcg	2700
OY	2816	GTGAGTGCACAGCATGAAGGAGGCAATCCTTCATATGACATAGTATAGCCAGCATTCAGCCCTC	2875
Db	2701	gtgagtgacagcagcatgaagagcaatctctcatatgacgttaactaagcaagcatctagccctc	2760
OY	2876	TCCATGGCATGATGCTGATCTGTAAAGCCATTGCAGAGATGTGTGTTCAGAGGGCAGC	2935
Db	2761	tcctatggcagtcacgtcgtacccctgaagaacatctcgagagtggtctcttgtcgaaggcag	2820
OY	2936	CTGGAGAGTCTCTCCGGCGTGCATGACGAGCGTTTCCGAAGATTCCTTCGAAGCCCTATG	2995
Db	2821	ctggagagcttctcccggtcgtcagctacagagcttctcgaagatctcttcgaagccctatg	2880
OY	2996	AAGTTTTTTCAGACGAGCCCCACAGGAGAGATTTCACAGCTTTCCTCAAGAAGACATGGAT	3055
Db	2881	aagttttttgacagcagaccaccaagggagagatcttccaagaagtttccaagaacatgatat	2940
OY	3056	GAAATTGACGTGGCGGCTGCCGTTCCAGGCCAGATGTTCATCCACAACGTTATCTGTG	3115
Db	2941	gaagttagcagtgcggtcgtctccagcgagatgttcatccagaaacgttatctcgtgtg	3000
OY	3116	TTTCTGTGTGGGAATGATCGAGAGAGTTCCTCCGTGGTTCTTGTGTGGCAGTGGGGCC	3175
Db	3001	ttctctcgtgtgggaatgaacgcgaagagcttctccgtgtgtctctgtgtgcagtgggccc	3060
OY	3176	CTTGTCATCCCTCTTTCAGTCTGCAGCATATGTCTCAGGGTCCCTATTCGGGACCTGAAG	3235
Db	3061	cttgtaacctcttcttcaagctccgcacatgtctccaggggtccgtatccggagactgaag	3120
OY	3236	CGTGTGACAAATATCACGACGATCACCTTCTCTCTCCACATCACCTCCAGCATACAGGC	3295
Db	3121	cgctctgacaataatcaacgcagtaaccttctctccacaatacgttccagatatacagggc	3180
OY	3296	CTTGCCGACCATCCACGCTCATCAATTAAGGGCGAGAGTTTGTGCACAGATATCCAGAGACTG	3355
Db	3181	cttgccacacatccacgcctacaataaaggcagaggttcttgcacaagataccaggaactg	3240
OY	3356	CTGTGATACAAACACAGCTCCTTTTCTTTTGTGTACGTGCGAGTCCGAGTGGCTGGCGTG	3415
Db	3241	ctgtgatacaacaagaagctctcttcttltgtttaaagtgatgcaagcggatggcgtgcgtg	3300
OY	3416	CGCGTGGACCTCATCAGCATCGCCCTCATCACACACAGGGGCTGTATATGTTCTTATG	3475
Db	3301	cggctggaacctatacagatcagtcgcccctacacacacaagggcgtgatatgcttctatg	3360
OY	3476	CAGGGCAGATTTCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGCCAGTTAAAG	3535
Db	3361	cacgggcagatctccccaagcctatgaggggtctcgcacatctcttatgtctccagttaaag	3420
OY	3536	GGGGTGTTCCAGTTTAAAGGTCAGACGTGGGATCTGAGAAAGAGTTCGATTTACTCGGTG	3595
Db	3421	ggggctgttccaagtttaacgttcagactcgtgagatcttgcaagaagatctgataltaacctcgtg	3480

QY	3556	GAGAGATCATCTACTACTATTAAAGCTCTGTCCTTGGAAAGCACCTCCAGATTTAAGAC	36555
Db	3481	gagagagcaatcacatcacatctaaagactctgtctcttggagcaaccttgcagaattagaac	35400
QY	3656	AAGGTCCTCCCTCCGTGACTGGCCCGAGAGAGAGAGTACCTTTGAGAACCCAGATG	37151
Db	3541	aaggtccctccctccctgactctgccccagagagaggtgactcttggagaacgcagagatg	36000
QY	3716	AGGTACGAGAAAACCTCCCTCTGTGCTTAAGAAAGTATCTTCAAGTCAAACTTAA	37755
Db	3601	aggtaccgagaaaaacccctctctgtctctaaagaaagtatctctcaagatcaaacctaa	36600
QY	3776	GAGAAATTTGACATTTGGGGGCGAGACAGATCGGGAATCCGCTGGGGATGGCCCTC	38355
Db	3661	gagaaagatctgcaatcttgaggggcggaagagatccgggaatccctcgaggagatgcccctc	37200
QY	3836	TTCCGCTCGGTGAGTTATCTCGAGGCTGCATCAAGATTGATGAGTGAATCAGTAT	38955
Db	3721	ttccgctctggtgaggtatctctggaagctgcatcaagattgtgaggtgagaaatcagtgat	37800
QY	3896	ATTGGCCTTGCCGACCTCCGCAAGCAATCTCTATATTTCTCAAGAGCCGCTGCTGTC	39555
Db	3761	attgaccttgccgacctccgaagcaaatctctatattccctcaagacgcggtgctgttc	38400
QY	3956	AGTGGCACTGTCAATCAATAATTGGACCCCTTCAACCACTACATCAAGAACAGATTGG	40151
Db	3841	agtgcacctgacagatcaaatcttggaccttcaaccagtatcaatcgyaagaccagatttg	39000
QY	4016	GATGCCCTGGAGAGGACACACATGAAAGATGTATTG	4052
Db	3901	gatgccctggagagagacacacaaagaaagattgctatgc	3937

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RESULT      5      US-10-172-086-81
; Sequence 81, Application US/10172086
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method and nucleic acids for the differentiation
; TITLE OF INVENTION: of prostate tumors
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/172,086
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 81
; LENGTH: 5881
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-172-086-81

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Query Match	64.8%	Score 3142;	DB 7;	Length 5881;
Best Local Similarity	78.5%;	Pred. No. 0;		
Matches 3774;	Conservative	0;	Mismatches 1035;	Indels 1;
				Gaps 1;
QY	10	TCGGAGCGCTGGTTAGGCGGCTGCGCGGTTCTCTGGACGCGGGCCAGGAAATTTCGA	69	
Db	91	tcggagagcgtyglttgagcggtctggcgcggttctgttttgatgagtaggggctgaaggaaattttga	150	
QY	70	TGTGAACCTAACAGTCTGTGTGAGCCCTGTGAACCTCCACTCAGAGGAAGATGAAGATATTCGA	129	
Db	151	tgtaaatctaatagtcttgagcttlttgaaattttattattagagaagaatcgaagatcatcga	210	
QY	130	CATGGGAAGAACGATATATCATCCGACGTCCTGGGTATGAGTGTGAGGAGAGAGAACGAG	189	
Db	211	tataagaaaagaatgataattattattttagtcttgggataagaagcttgagggagaagaattag	270	
QY	190	CACTTTCTGGAGCGCACAGAGACCGGTGAAGATTCCAAAGTTCCAGAGAGAACCTGCACCGCTTGA	249	
Db	271	tatttttgagcgctataaagaatcgtgaagaattttaagtcttgaagaatctcaatcatttga	330	

QY	250	ATGCCAAGATGCGCTTGGAAACACACACC	CGGACCGCAAGGGCCCTCTCTTTGATGCGCTCAT	309
Dp	331	atgttaagaatggttttggnaa	tagtctcgaaatcgagggtttttttttttagtctttat	390
QY	310	GCATTCACAGTCAGAAATCCTGGATGAGG	AGCATCCCAAGGAAAGTACCATCATGCGCTT	369
Dp	391	gtattcttagtttagaattcttggaa	tcttggaaagtaattttaaagataatcatagttc	450
QY	370	GAGTGCCTCAAGCCCATCCGAGCTACT	GTTCGCAAAACACACGACCCAGTGGACAAATCGCG	429
Dp	451	gagtgcttttgaagttaattatc	gagataattttaaataatagataattagtgabataatgttg	510
QY	430	GCCTTTTTCCTGTATGACATTTTTCGTG	CGCTTCTCTGCGCGGTGAGCCCAACAGAA	489
Dp	511	gtctttttttttagatgttttttcg	tggttttttttttttttttttttttttttgcgttgattaa	570
QY	490	GGGGGACCTCTCAATGGAAACAGCTG	GTGTCCTGTCCAAAGCAGAGTCTTCTGACGTGA	549
Dp	571	gggggagtttcttaatgnaa	acgctgtgttttgtttaaagtaagatttcttgcagtgaa	630
QY	550	CTGCAGAGAAGCTAGAGAGACTGTG	CGCAAAAGAGCTGAAGTGTGGGCCAGACGCTGC	609
Dp	631	tctgtaagaagattgagagatctg	tgtaagaagaatgttgaaatgtttagaagctgtg	690
QY	610	TTCCCTCGAAGGCTGTGTGATCTTCT	TGCGCCAGCACAGGCATCATCTGCATCGTGTG	669
Dp	691	tttttctggaagggtctgtgtg	gtgttttttgcgtattagttattcttgcattacgtgtg	750
QY	670	CCCTATATACGACAGCTGGCTGGCT	CTTCAGATGGACAGCCTTCATGTGTGAACACTCTT	729
Dp	751	tttgaatattacgtagtctgtgtgtt	gtttagtgatagttttaa	810
QY	730	GGAATATACCAGGCAACAGACAGT	CTTAACCGCATCGCTGTGTGTTAGTGGCGGCT	789
Dp	811	ggagtaattatagtaataagat	ttaattctgtatagatagttgtgtcttagtggttgc	870
QY	790	CTTCCTGACGGAATCGTGGCGTCT	TGTGTCGTGCATGACTGAGGCAATTGAATTACCG	849
Dp	871	tttcttgaagaaatcgtgtgtgt	ctgttgcgtttttagtatttggttgagcttgaattacg	930
QY	850	AATCGGTGTCCGCTTCGCGGGGGCC	ATCTTAACCATGGCATTTAAGAAAGATCCTTAAGT	909
Dp	931	aactcgtgtctgtctgtgcgggggt	ttaattcttaattctgtattctgaagaagattttaaagt	990
QY	910	AAACAACTTTAAAGAAATCCCTGG	TGAGGCATCAACATTTGCTCCCAACGATGGGCA	969
Dp	991	aagaaataataaagaagaattt	tttgggtgaatttaataatctgttttaaagaaaggta	1050
QY	970	GATATGTTTAGGACGACGACCCG	TGTTGGACCGTGTGAGGACCCGATGTTGGCAT	1029
Dp	1051	gagaaatgtttgagtagtagtctg	tgttagttgtgtgttgtaggaattcgttgtgtat	1110
QY	1030	CTTAGCATATTTATATGTAAATT	TTTTCGGACCAACAGGCTTCTTGGGATCAGCTGT	1089
Dp	1111	tttagtataatlaataatlaata	tattcttggatlaaagtttcttggagtaagtgt	1170
QY	1090	TTTTATCTCTTTTACCACCAATG	ATGTTGGTACAGGCGTCAGACAGATTTTCAGAGG	1149
Dp	1171	tttatttttttattatattag	taagtgtctgtattatcaaggttataagataatttaagag	1230
QY	1150	AAAATGCGTGGCGCCAGCGAT	GAAGTGTCCAGAAAGATGAAGTCTTACTTACAT	1209
Dp	1231	aaaatgctgttcgttatag	taagtaacgtgttttagaagatgaatgaagtttattat	1290
QY	1210	TAAATTTATCAAAATGTATGCT	CTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAATCG	1269
Dp	1291	taaatattatataaagtatgt	tttgcgttlaaaglatatttlltagagctgtlltagaanaatc	1350
QY	1270	CGAGAGAGACGTCGGAATTTGG	AAAAAGCGGGGTCTTCCGACATCAACGTGGGCTGT	1329
Dp	1351	cgaagagagagcgtccgata	ctatgaaaaagtcgggtatctttagagataltatgttgcgtg	1410
QY	1330	GGCTCCCATTTGTGGTGATGTC	CCAGCGGTGTGACCTTCTGTTCATATGACCTCGG	1389

Db	1411	ggtttatttctgtgtgtgattctgtacgtygtgattcttttctgttatatgatttggg	1470
Oy	1390	CTTGAGATTGTGACACACACAGCGCTTTTCACAGGGTGAGACGTTCAATTCATGACTCTT	1449
Db	1471	tttcgattctgtatgtatataagtttcttatagtgtgtgaagttcttaatttatgattctt	1550
Oy	1450	TGCTTTGAAAGTAAACACCCTTTTCAGTAAAGTCCCTTCAGAAAGCCTCAGTGGCTGTGA	1509
Db	1531	tgttttgaagtaataatcgtttcttagtaaaagtttttttagaagtttagtgtgttga	1590
Oy	1510	CAGATTTTAAAGATTGTTCTTAATGGAAGGTTTCATGATTAAGAACAAACACCCAG	1569
Db	1591	tagatttaaggttctgtttttaaagtgaagaggttttatatgataaagaataattagtag	1650
Oy	1570	TCTTCACATCAAGATTAAGATGAAAGAAATGCAACCTTGAGAGGGAGCTCCTCCACTCCAG	1629
Db	1651	ttttatatattaagaatagaatgataaaatgtatttttggatagggattcttttattcttag	1710
Oy	1630	TATCCAGACACCTGGCCAGCTGACCCCCCAAAATGAAAAAGACAGAGGGCTTCCAGGGG	1689
Db	1711	tatttagaattcgttttaagttagttttttaaatagaaaaagataagaggtttttagggg	1770
Oy	1690	CAAGAAAGAGAAGGTGAGCAGCTGACGGCACATCGATCAGGGGCTGTGCGAGACA	1749
Db	1771	taagaagaagaagtygagtyagttctagcgtatgtatgataagcgtgtctgtataga	1830
Oy	1750	GAAAGGCCACTCTCTCTGTGACAGTACAGACGCGGCCACTCCCGAAGAGMAAGACAA	1809
Db	1831	gaagagttatttttttcttgatagtgacagagcgttttagttcgaagaaggaagaagttaa	1890
Oy	1810	GCATATCCACCTGGCGCCACTGGCTTACAGAGAGACATGCGACACATTCGATTCGAGAT	1869
Db	1891	gtataattatttgggtatttctgtttatcttagatagaagatattgtatagcgttcgattggagat	1950
Oy	1870	CCAAAGGGTAAACTGGTGTGGAATCTGCGGACAGTGTGGAGATGGAAAAACCTCTTCAT	1929
Db	1951	ctaaagaggttaaatctgttgaaattctgcgttagtctgtggaagctggaataatttttat	2010
Oy	1930	TTTCAGCATTTTACGCCAGATGACGCTTCTACAGGGCCACCATGGAATTCATGGAACTT	1989
Db	2011	tttagtatttttagtttagatagatgcgtttttagagggtagtattcttaatttagtgaaattt	2070
Oy	1990	CGCTTATGTGGCCAGCAGACGCTGGAATCCATAGCTACTCTGAGAGACAACTACTGTT	2049
Db	2071	cgttaatgtgttagtagtaggtttggaattttaaagtatttcttgagaagataatatttgct	2130
Oy	2050	TGGGAGAAGATATGATGAAAGAAATACAACTCTGTGCTGAACAGCTGCTGCTGAGGCC	2109
Db	2131	ctggaagaagaataatgataagaagaataataatttctgttgtaagtgtgttgtagagtt	2190
Oy	2110	TGACCTGGCACTTCTTCCGACGACCACTGACGAGATTTGAGAGCGAGAGCCAACT	2169
Db	2191	tgatttggttatttttttcttagtagcgaatttgaagagatcttgagaagcagagattaaatt	2250
Oy	2170	GAGGAGGAGGAGGAGCGCAAGAGATTCAGCCCTTGCCGGCTGTATAGTCAGAGAGCAT	2229
Db	2251	gagcggtygggttagcgttagagaagataagtttctgtcgggttttgatatagtatagaagat	2310
Oy	2230	CTACATCTGTGACAGACCCCTCTCAGATGCTTGAATGCGCCATGTGGGCAACCACTTTCAA	2289
Db	2311	ttataatttggagaattttttagtgttcttagagtggttagtggtggttaattatatttttaa	2370
Oy	2290	TAGTGTCAATCCGGAACACTCTCAAGTCCAAAGACAGTCTGTTGTTTACCACACTGTACA	2349
Db	2371	tagtgttattctggaataattttaaagtttaagataagtttctgttcttatattatagttata	2430
Oy	2350	GTACTCTGGTTACAGTATATAAGTGAATCTTCATGAAAGAGGCTGTATATTCAGAAAGAG	2409
Db	2431	gtatttggttgattctgtatagaagtgtatttcttagaagaagggtctgtatatacggaaagag	2490
Oy	2410	CACCATGAGAGACTGATGAATTTAAATGATGCTACATTTTAAATTAACCTGTT	2469

Dh 2491 tattatagaggaaatgataaatttaaaatgagatgattatatttataaattgtt 2550
Oy 2470 GCTGGAGAGAGACCGCCGATTGAGATCAATTCAAAAGAAACCAGTGTTCACAGAA 2529
Dh 2551 gtgggagagataatgattgattgatttataaagaagaattagtggttataaaga 2610
Oy 2530 GAAGTCACAAAGCAAGGGTCTTAAACAGATCAATAAAGAAAGAAAGCAAGTAAAGCC 2589
Dh 2611 gaattataagaataagggttttaaaataagattagtaagaagaagaagtaagaagt 2670
Oy 2590 AAGAGAGAGGACGCTTGTGACCTGAGAGAAAGGCGAGGTCAGTCCCTGGTCAAT 2649
Dh 2671 agaggaagaggtatgttgtagtggaagaagaaggtagggttagtggttgtagt 2730
Oy 2650 ATATGCTGTCAATCCAGGCTGTGAGGGCCCTTGGCATTCCTGTTATTTAGGCGCT 2709
Dh 2731 atatgtgttattatattagtggttggtgggtttttgtgatttttggttataatggtt 2790
Oy 2710 TTTGATGCTGAATGTAGGACGACCGCTTCAGCACCTGGGTGTTGAGTTAGTCGATCA 2769
Dh 2791 tttaattgtgaatgttagttagtattttagtatttggttggttagtattgattaa 2850
Oy 2770 GCAAGAGAGCGGGAACACACTGTGACCTGAGAGAAACGAGACCTCGGTGATGACAGAT 2829
Dh 2851 gtaaggaagcgaggaataattatattgtaattcgaggaacgagattcggtgagtgatag 2910
Oy 2830 GAAGGACATCCTCATATGACGATCTATGACGATCTACGCTTCCATGAGTCAAT 2889
Dh 2911 gaaggaataatttatattgattagttatgattagttatgatttatttattatgattat 2970
Oy 2890 GCTGATCTGAAAGCATTCCAGAGAGTGTCTTGTGCAAGGCGACGCGAGCTTCTTC 2949
Dh 2971 gtgatttgaagttatcgagaggttggtttgttaaggatcggttcgaggtttttt 3030
Oy 2950 CCGGTGATGACGAGCTTTCGAGAGATCTCTGAAAGCCTTGAAGTTTGTGACAC 3009
Dh 3031 tcggttgtagcagaggttttcgaggaagatttcggaattttagaagttttttagaac 3090
Oy 3010 GACCCCCACAGAGAGATTTCTCAACAGSTTTTCCAAAGACATGATGATGAGTCACTCG 3069
Dh 3091 gattttatagggagatttttaataagtttttaaaagatatgataagttgaagtcg 3150
Oy 3070 GCTGCGGTCCAGGCGGAGATGTTTCATCCAGACGTTATCTGTGTTCTTCTGTGGG 3129
Dh 3151 gtctgctttagtgcgagatgttatttagaagttatttgggttttttgggtg 3210
Oy 3130 AATGATCCAGAGATCTCCCGGTGTTCTGTGTGACATGGGCCCCCTTGTCACTCTCT 3189
Dh 3211 aatgacgtgaaggttttcgtgtgttttggtagtggtgttttggattttttt 3270
Oy 3190 TTTGATCCTGACATTTGCTCCAGGATCTGATTCGAGGAGCTGAAAGCTGACATAT 3249
Dh 3271 tttagttttagtattgtttttaggttttagtattcggaagttgaagtcgttgaataat 3330
Oy 3250 CAGGACATGACCTTCTCTCCATCCAGATCCAGATACAGAGGCTTTCACCATCA 3309
Dh 3331 taatgttatt 3390
Oy 3310 CGGCTACAAATTAAGGAGAGGATTTGCAAGATACAGAGAGCTGCTGATGACAAACA 3369
Dh 3391 cgtttaataaataaggtagaggttttctgtagaataatagaagttgtgtagtaataa 3450
Oy 3370 AGCTCTTTTTTTTTTTTAACTGATGAGGATGCGGTGCTGCGGCTGAGACATCAT 3429
Dh 3451 agtt 3510
Oy 3430 CAGCATGCGCCTCATCAACACAGGAGGATGATGATGATGATGATGATGATGATGATG 3489
Dh 3511 tagatcgttt 3570
Oy 3490 CCGAGCTATGCGGCTGCTGCGCATCTTATGCTGCTCAAGTTAAAGGCGCTTCCAGTT 3549
Dh 3571 tttagttatgaggttctgttatttttttttttttttttttttttttttttttttttttt 3630

Oy 3550 TACGGTCAGACCTGGGATCTGAGACAGAGCTGATTCACCTGGTGGAGAGATCAATCA 3609
Dh 3631 taaggttaagatcgtgataatcgtgaagaaagttatatttcgttgagagattaaatca 3690
Oy 3610 CTACATTAAGACTCTGTCTGTAAGACACCTGCGACAGATTAAGAACAAAGCTCCGCC 3669
Dh 3691 ttatattagattttgttttttgaagttattgttgaatattgaataaagaattttttttt 3750
Oy 3670 TGACTGGCCCCAGAGAGAGAGAGTGAACCTTTGAGAACGACAGATGAGGTACCGAGAAA 3729
Dh 3751 tgattgtttttagagagaggttgattttttagaagcgttagagtagaggttalcggaanaa 3810
Oy 3730 CTTCCCTCTGCTCTTAAAGATATCTTCAGATCAACCTTAAAGAAATATGAGCT 3789
Dh 3811 ttttttttcgttttaaaagaatttttttcagataaatttaagaagaagattgtagt 3870
Oy 3790 TGTGGGCGGACAGATCAAGAGAGTCTGCTGGGAGATGGCCCTTCTGCTGATGGA 3849
Dh 3871 tgggggscgagatagattagtaggaagtttcgttgggagatgttttttcgtttgtaga 3930
Oy 3850 GTTATCTGAGGCTGCATCAAGATTGATGAGTGAAGATCAATGATGATGATGATGATG 3909
Dh 3931 gtatttgaggttattatgaattgtagtgagtggaattagattgattgttgcga 3990
Oy 3910 CTTCCGAGCAACCTCTATCATTCCTCAAGAGCGCGGTCTGATGAGTCACTGCTCAG 3969
Dh 3991 ttttcgaagtaaatcttattattattttaaagagtcggtgtttagttagttagttag 4050
Oy 3970 ATCAAAATTTGAGACCCCTTCAACACAGTCACTCAACACAGATTTGGATGAGCCCTGAG 4029
Dh 4051 ataaatttggttttttttaatttagtatattgaagaattagatttggttggtttggaag 4110
Oy 4030 GACACATGAAGAAATGATTTGCTACGCTACCTGAAATCTGAATGATGATGATGATG 4089
Dh 4111 gatataatgaagaatgattgtttagtatttttgaatttggaatttggaattgtaga 4170
Oy 4090 GAATGGGAGTAACTCTGATGAGGAGAGCGAGCTCTTGTGCAATGATGAGCCCTCT 4149
Dh 4171 gaaagggatattttttagtgaggagagaggttttggtagttagttagttagttagttagt 4230
Oy 4150 CCGGACATGATGATTTGATGAGAGCCACAGCTGCGATGCGACAGACAGACA 4209
Dh 4231 tegtattcgttaagatttttagtatttagatgaagttatagttttagttagatagaataga 4290
Oy 4210 CTATTTGATTAAGAGACATTCGAGAGATTTGACAGCTGATCAATGATGATGATGATG 4269
Dh 4291 ttattgatttaagaagattatcgtgaagattttttagttagttagttagttagttagttagt 4350
Oy 4270 CCATGCGCTGACACAGGTTTAAAGTCCGATTAAGATTTAGTGTGCTGCGCCAGGACAGT 4329
Dh 4351 ttatcgtttgtataagttttaggttttagatagaattagttgtgtgtttaggagtaggt 4410
Oy 4330 GGTGAGATTTGACACCCCATGCTGCTTCTGTCACAGACAGGTTCCGATCTATGCAAT 4389
Dh 4411 ggtgaggtttagatatttttagtattttagttttttagaagatagttttagtatttagttag 4470
Oy 4390 GTTGTGCTGCTCAGAGAAAGGTCGCTGCAAGGCGTGAACCTCTGCTGAGAGAT 4449
Dh 4471 gttcgttgtagaagaataagtcgttttagaaggtttagtattttttttttttagcgaagt 4530
Oy 4450 CTCTTTTCTTAAAGCATTTGCAATTCCTGCTGGGCGGCGCCCTTCAATGAGTCTCTCC 4509
Dh 4531 ttttttttttagagattttagtattttttagttgttggtggcggtt-tttttatcgcgttttt 4589
Oy 4510 TACGAAACCTTGCTTCTGATTTTATCTTGTGACAGACAGATTCGAGATGAGTCTGCTG 4589
Dh 4590 tatcgaatattttagtttttttcgatttatttctgtagtagtagttagttagttagttagttag 4649
Oy 4570 TGTTCATTTTAAAGAGAGTCAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTT 4629
Dh 4650 ttttttttttttagggagtagtatttttagtatttttagtattttattattattatttagttag 4709

[illegible]

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RESULT      6
US-10-172-086-82/c
Sequence 82, Application US/10172086
GENERAL INFORMATION:
APPLICANT: EpiGenomics AG
TITLE OF INVENTION: Method and nucleic acids for the differentiation
TITLE OF INVENTION: of prostate tumors
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/172,086
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 82
LENGTH: 5881
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-172-086-82

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Query Match	62.1%	Score 3011;	DB 7;	Length 5881;
Best Local Similarity	76.7%;	Pred. No. 0;		
Matches 3697; Conservative	0;	Mismatches 1125;	Indels 1;	Gaps 1;

OY	4	TCATGCTCGGGAGCGTGGTTGACGGCTGGCGCGGTTCCTCGAGACGAGGGCGCGAGAA	63
Db	5797	TAAATCTCGAAAGGTAATTAATTAAGAGACTAACGGATTAATCTTAAACACAAAACGGAAAAA	5738
OY	64	TTCTGATGTGAACCTAACACTCTGTGAGCCCTGGAACTCTCACTCGAGAGAGATGAAGA	123
Db	5737	TTCTAATATATAAACTATACATCTATATAAACCTTAAACCTTCACCTCAAAAAAATAAAAA	5678
OY	124	TATGACATTCGAGAAAGAGTATATCATTCCTCCAGTCTGGGTATGAAAGTGCAGGAGAG	183
Db	5677	TATGACATTAATAAAAAAAAAAATATCATCCCACTCTAATATATAAAATATATAAAAAA	5618
OY	184	AACGAGACTTGTGGGAGCGACAGAGACGGTGAAATTCAGAGTTGAGAGAACTCGAC	243
Db	5617	AACCAACACTTCTTAATAACGACACAAAAACCGTAAAAATTTCCAAATTCAAAAAAACTCGAC	5558
OY	244	GTTGGAATGCCAAGATGCTTGGAAACAGAGCGCGAGCGGAGGGCGCTCTCTTGATGC	303
Db	5557	GTAAAAATACCAAAATACCTTAATAAACCAACACCCGAAACCGAAAAACCTCTCTTAATAC	5498
OY	304	CTTCATGCAATTCAGCTCGAATTCCTGGATGAGAGCATCCCAAGGGAAGTACCATCA	363
Db	5497	CTTCATGCAATTCCTAACTCAAAATCTTAATTAATAAAACATCCCAAAAAAATTACCATCA	5438
OY	364	TGGCTAGAGTCTGAAAGCCATCTCGGACTACTTGCAAAACACAGACACCCAGTGCACA	423
Db	5437	TAACTTAATTAATCTATAAACCATCCGAATCTACTTCCAACACACACACCCCAATTAACAA	5378
OY	424	TGCTGGCGCTTTTTCCTGTAAGACTTTTTCGTGGCGTTCTCTCTGGCCCGTGTGGCCA	483
Db	5377	TACTTAACCTTTTCCATTAATTAATCTTTTTCGTAACCTTTCTCTCTCAACCCGATTAACCA	5318

OY	484	CAAAAGAGGGGAGCTCTCAATGSAAGACGTGTGTCTCTGTCCAGCAACGAGTCTTTCGA	543
Db	5317	CAAAAAAAGAACTCTCAATATAAAAAAGCTATTAATCTATCTATCCAAACGGAATCTTTCTAA	5258
OY	544	CGTAACTGGAGAAGACTAGAGAGCTGGGCGCAAGAAGCGTGAATGAATGGGCGCA	603
Db	5237	CGTAAACTACAAAAAACTAAAAAACTATACAAAAAAACTAAATTAATAATTAACCAA	5198
OY	604	CGCTGTTCCCTGCGAAGGGGTGTGTGATCTCTTCTGCGGACACAGGCTCATCTGTCCAT	663
Db	5197	CGCTACTCTCCCTAGAAAAATTTATTAATTCCTTACCGCACAAACTCATCTATCCAT	5138
OY	664	CGTGTGCTGATGATCAGCAGCTGGCTGGCTTCACTGGACACGCTTCATGTGGAAACA	723
Db	5137	CGTATACCTATATATACCGCAACCTAACTCAATCAATAAACCAACCTTCATATAAACA	5078
OY	724	CCCTTGAGATATATACCGGCAACAGATCTTAACCGGACGTACAGCTGTGTTGAAGGCT	783
Db	5077	CCCTGTTAAATATATACCAACAAACAAATCTAACCCTACATATCAACTTATTTATATACT	5018
OY	784	GGGCGCTCCTCTGACGGAAATCGTGGCGTCTTGTCGTGTCACATGACTTGGGCAATTGAA	843
Db	5017	AAACCTCCTCTTAACGAAATCGTACGATCTTAATCGGTACACTAAGCTTAAAGGTTAAA	4958
OY	844	TTACCGAACCGGTGTCCGCTTGCGGGGGCCATCCTAACCATGCAATTTAAAGAATCTCT	903
Db	4957	TTACCGAACCGAATCCGCTTACGAAAAACCATCTCAACCATMACTTTTAAAAAAATCT	4898
OY	904	TAACTTAAAGACATTTAAACGAATCCCTGGGTGGTGCATCAACATTTGCTCCACGA	963
Db	4897	TAAATTTAAAAACATTTAAAAAAATCCCTAAATTAATCAATCAATCAATTTACTCCACGA	4838
OY	964	TGGGCAAGAGATGTTTAGGCGACAGCCGTTGGACCGCTGCTGGGTGGAGAACCGGTGT	10233
Db	4837	TAAACAAAAATTTTAAACAACACCGTTAAACAACCTACTAAGTAAAAAACCGGTAT	4778
OY	1024	TGCCATCTTAGGCATGATTTATATGATTAATTTCTGGAGCCACAGGCTTCTGGGATC	1083
Db	4777	TACCATCTTAAACATATTTATTTATTTATTTCTTAAACCCMACAACTTCTTAAATCT	4718
OY	1084	AGCGTTTTTATCCTCTTTACCACAGCANTGATGTTGATAGGCGTCACAGCATATTT	1143
Db	4717	AAGATTTTTTATCCTCTTTTACCACCAACAAATATTTACATAGAGCTCACACATATTT	4658
OY	1144	CAGAGAGAATGCGTGGCGCCGACAGGATGACGCTGTCCGAAGATGAATGAAGTCTTAC	12033
Db	4657	CAAAAAAAATACGTAAACGCCGACGAATAAAGCTATCCAAAAAATATTAATAATTTCTTAC	4598
OY	1204	TTACATTTAAATTTATCAAAATGTATGCTTGGGTCAAGCATTTTCTCAGAGTGTACAA	12633
Db	4597	TTACATTTAAATTTATCAAAATGTATGCTTAAATCAAAACATTTTCTCAAAATATTCAAA	4538
OY	1264	AATCCGAGAGAGAGCGGTGGGATTTTGGAAAAAGCCGGGTACTTCCAGAGCATCAGT	13233
Db	4537	AATCCGGGAAAAAAGAGTGGAAATTTAAAAAAAACCGAATCACTTCCAAAACATCAGTAT	4478
OY	1324	GGGTGGGCTCCCATTTGGTGGTGAATGCGACGCGTGGAGCTTCTCTGTTCATATGAC	13833
Db	4477	AAATATATACCTCCATTTATATATTAATTAATACCAACGTAATATACCTTCTCATATATAC	4418
OY	1384	CCTGGGCTTGATCTGACAGCAGCAGAGGCTTACAGTGGTGAAGTCTTCAATTCAT	1443
Db	4417	CCTAAACCTTGATCTACCAACACAAACATTTCAACAATAATTAACAATCTTCAATTCAT	4358
OY	1444	GACCTTTGCTTGAAGTAAACACCGTTTTCAGTAAGTCCCTCTCAGAAGCCTCAGTGGC	1503
Db	4357	AACCTTTACTTTAAATAATACCGGTTTCAATTAATCCCTCATAAAACCTCATATAC	4298
OY	1504	TGTTGACAGATTTTAAAGTGTGTTTCTTAATGAAGAAGGTCTACATGATATAAGAACAAAC	1563
Db	4297	TATTAACAAATTTTAAAAATTTATTTCTTAATTAATAAAAAATTTCAATATATTAACAAAC	4238
OY	1564	AGCCAGTCTTCACATCAAGATAGAAAAATGCCACCTTGGCATGGGACCTCTCCCA	16233

Dh 1124 agagggccatcagctctcaccggtgatgtaaacctcgtttgaaagggtgtgctatgg 1183
Qy 997 GAGCGCGTGGCGTGGAGAGACCCGTTGTCCTGCAATCTTAGCAGATGATTAATAT 1056
Dh 1184 acccttaagtaactgatacctgcatcgctgtcattcgtcagcattcttctactcat 1243
Qy 1057 TCTGGGACCAACAGAGGCTTCTGGGATCAGCTCTTTTATCTCTTTTACCAGCAATG 1116
Dh 1244 tatgtatacactgcatctattgtccactatgcatctccctgtgttccctcgtggct 1303
Qy 1117 GTTTCATCAGCGGCTCAGCAGCATATTTCAGGAAAAATCGTGGCCGCCAGATGAC 1176
Dh 1304 atctatgacaagaatgctgtgtaaggctcagatcacacatctgtggtcagcagcag 1363
Qy 1177 TGTCCAGAGATGATGAAAGTTCTTACTTACATTAATTAATCAAAATATAGCCGTG 1236
Dh 1364 cctccgtgtgaccagtgtaagttcctcattgcatctgcatatgaatgtaacactgg 1423
Qy 1237 CAACGCAATTTTCTCAGAGTGTTCAGAAAAATCCGAGAGAGCGCTGGATTTGGAAA 1296
Dh 1424 gaacacatttgcaaaaaatcatatgaaagcctaagaagaaagaaagaaactttggaga 1483
Qy 1237 AGCCGGTACTTCCAGAGCATCTGTGGGTGGCTCCCATTTGTGTGTGATTTGCCAG 1356
Dh 1484 gtgcgggtgtgtccagagccttgacaagataaactgttcatcatctccacagtgccac 1543
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Qy 1417 CACAGTGTGACAGTCTTCAATTTCCATGACTTTTGTGAAAGTAAACCGCTTTTCA 1476
Dh 1604 cagcagctgtgctccttgaatctcctcctcgtcgtcagtgctgtccttctgtccattg 1663
Qy 1477 AAAGTCCCTTCAGAGAGCTCAGTGGCTGTGACAGATTTAAGATTTGTTCTAATGA 1536
Dh 1664 caaaggtctcagaattcacaagctcgtcagtgatgagttcagaaggttttctccagga 1723
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Qy 1537 TGCCACCTTGGCATGAGGAGCTCTCCACCTCAGATTCAGAACTGCCCAAGCTGAC 1656
Dh 1784 ggcacactgtcattgacacagacgtgtccggggtc----- 1820
Qy 1657 CAATATGAAAAAGCAGAGAGGCTTCCAGGGGCAAGAAAGATGAGGACAGCTGCA 1716
Dh 1821 ----- 1820
Qy 1717 GCGCATGAGCATGAGGGGTGTGGCAGAGCAGAAAGGCCACCTCCTGCTGACAGTGA 1776
Dh 1821 -----gtcaatggtggtcgtgagctgtgagaaagaaagcgtcttctgaaagaa 1873
Qy 1777 CGAGCGGCCCGCTCCGAGAGGAAGAGAGCAGCATTCACCTGGGCACTGCGCTT 1836
Dh 1874 cagcgtctagagatgcctccggtccaggaagaaagaaagcagctggtccagag----- 1928
Qy 1837 ACAGAGGACATGACAGCATGATCTGAGATTCAGAGAGGATAACTGTGTAATGTG 1896
Dh 1929 -----ttgcacaagaatcaactgtgtgtgtccaaaggtgatagttttaaggtgt 1978
Qy 1897 CGGCAGTGTGGAGATGGAATAACCTCTCATTTTCAGCCCTTTTAGGCCGATAGAGCCT 1956
Dh 1979 cggagaaacaggggtgtgtaagagcagcgtgtgtcagccatccctggagaggaatgac 2038
Qy 1957 TCTAGAGGACAGCATTCATCACTGGAACCTTGCTTATGTGGCCAGCAGCGCTGTAT 2016
Dh 2039 gctcaggggtcgtgtggtgtgaggaagcctgtgtctatgtccccaagcagcgtgat 2088
Qy 2017 CCTCAATGCTACTGTGAGAGCAACATCTGTTTGGAGAGAAATATGATGAAGAAAGATA 2076
Dh 2099 cgtcaagggagaaacatcagggagaaacatctcatgtgaggtgcataatgaaagccgata 2158

Qy 2077 CAACCTGTGTGACAGCTGCTGCTGAGAGCCCTGACCTGGCCATTCTTCCAGCAGCA 2136
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Qy 2137 CCTGAGCGATTTGGAGAGCAGAGACCAACCTGACAGGCTGGGCAAGCATCAG 2196
Dh 2219 catgacaagaatggaagagcgggtcctcaacctctctggtgggggcagaaacagagatac 2278
Qy 2197 CCTTGGCCGGGCTGTGATAGTGACAGAGCATCTCATCTCTGAGAGACCCCTCGTGC 2256
Dh 2279 cctggcccggtcgtgtatctccagcgttcagatctacccctgtgagagacccctgtgtc 2338
Qy 2257 CTTAGATGCCCATGTGGGCAACCACTTTCATTAATGCTGCTCGGAAACATCTCAATC 2316
Dh 2339 tgtgagcgcacagtggtggaagacacattttgaggtgtgatttaagaagaacatcaggg 2398
Qy 2317 CAAGCAGTTTGTGTTGTATACCAACAGTTACAGTACCTGTGTGACTGTGATGAATG 2376
Dh 2399 gaagaggtcgtcctgtgtgagccacagctgagtaactagaatttgtgtccagatcat 2458
Qy 2377 CTTATGAAAGAGGCGCTGATTTACGGAAGAGCAGCCCATGAGAACTGATGATTTAA 2436
Dh 2459 ttgtgtggaataatggaataatctgtgaaatggaactcagctgtgttaatgtcagaaaa 2518
Qy 2437 TGTGACTATGCTTACCATTTTAAATACCTGTTGCTGGAGAGACCGCGAGTTGAGAT 2496
Dh 2519 ggggaataatgcccaactatccagaagaatgcagaaggaagcacttgagacatgtga 2578
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Dh 2579 ggaacacgaagaataagcagagaagccaaaggtagaagctcgtccacatccct 2638
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Dh 2639 ggaagagctctcacaaggaatgctgt-----gcggagatcaagctcacaacagga 2692
Qy 2617 AGAGAAAGGCGAGGTTAGTCCCTGCTGACGTATATGCTGTCTCATTCACAGCTGTGG 2676
Dh 2693 ggaagatggaagaggtcctctgtgagtgaggtgtctacacacatcattcaggtcagctg 2752
Qy 2677 GGGCCCTTGGCATCTCTGTTATATGAGCCCTTTTCATGTTGATGAGGACAGACCGC 2736
Dh 2753 aggttaactgtctcttgacataatttctctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2812
Qy 2737 CTTACGACCTGTGTGTTAGTTACTGATCAAGCAAGAAAGGCAACCACTGTGAC 2796
Dh 2813 ctacagctctgt 2872
Qy 2797 TCGAGGAAGCAGAGACC-----TGGGTGAGTGACAGCATGGAAGCAATCTCATATGCA 2853
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Qy 2854 CTATGCCAGCATCTACGCCCTCTCCATGAGCAGTGTGATTCCTGAAGCAATTCGAGG 2913
Dh 2933 ctacagctgt 2992
Qy 2914 AGTGTCTTGTGCAAGGCGACGTGCGAGCTTCTCTCCGCTGCAATGACGAGCTTTTCCG 2973
Dh 2993 aggaatttccacaaagatcagaagaaagcattccacggtcctgcacaacagcttctaa 3052
Qy 2974 AAGGATCTTGGAAAGCCTATGAAGTTTTCACACGACCCCGCAGGAGGAGATTTCAA 3033
Dh 3053 caaagtttccgt 3112
Qy 3034 CAGGTTTCCAAAGACATGATGATGAGTGTGAGTGTGGCTGTGCTTCCAGCGCGGATG 3093
Dh 3113 ctgtctgtcaggggaactgtggaacagctgtgacacgtctgtgtgtgtgtgtgtgtgtgt 3172
Qy 3094 CATCCAGAACGTTATCTGTGTGTTCTTGTGTGTGGAATGATCCAGAGAGTCTTCCG 3153
Dh 3173 cctgtctgt 3252


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; NAME/KEY: misc_feature
; LOCATION: (927)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-137-337-228

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Query Match	12.2%	Score 591.8;	DB 7;	Length 1579;
Best Local Similarity	99.5%;	Pred. No. 4.1e-104;		
Matches 604;	Conservative	0;	Mismatches 2;	Indels 1;
				Gaps 1;

OY 4213 ATTGATTCACAGACCAATCCGAGAAAGATTGACAGCTGTACCAATGGCGACCATTTGGCCA 4272
 Db 1 atcatctcaaaagaccacccgagaagaactcttgcagactctgataccatctgcgaccatctgcga 60
 OY 4273 TCGCCTGCACACGGTTTCTAGGCTCCGATAGGATTATGCTGTGGCCACAGGACAGTGGT 4332
 Db 61 tcgcctgcacaacggtctcttagcttcgataagattatgtgtgtgccccaggaagtggt 120
 OY 4333 GGAGTTTGACACCCCATTGCTGTCTTCTGTCCACAGACAGTTCCCGATTCTATGCCATGTT 4332
 Db 121 ggaatttgcaccccacatctgctctctgtccaaagaaagttcccgattctctatgcgaagtt 180
 OY 4393 TGGCGCTGCACAGAACAAAGGTCGCTGTCAAGGGCGACTCCTCCCTGTGTGACGAAGTCTC 4452
 Db 181 tgcgcctgcacaagaacaaagtcgcgttcaaggctgcactctccctgttgcagaagttc 240
 OY 4453 TTTTCTTTAGAGCATTTGCCATTCCCTGCTGGGCGGGCCCTTCATCGAGCTCCCTCTAC 4512
 Db 241 tttctcttagagcaatgcatctccctgctggtggcgggcccc-tgactggtctctctac 299
 OY 4513 CGAAACCTTGCCCTTCTCGATTTTATCTTCTTGGCACAGACAGTTCGAGATTGGCTGTGTGT 4572
 Db 300 cgaaacctgtcctctctgattatctcttgcacaaagactccggaattggtctgtgt 359
 OY 4573 TTTCACTTTTAGGAGAGCATATTTTGTATTTGATTATTTTCCATATTTCATGTAACAA 4632
 Db 360 ttcactcttagggagagcatatcttgaattctgtattatctcatatctctgtaaaaaa 419
 OY 4633 AATTAGTTTGTGTTTAATTATGACCTCTAAAGGTTCCAGGAAACCGTTATTATTAATTGT 4692
 Db 420 aatttagttcttgccttcttaattgcactctaaaggcttcagggaaccttataattgt 479
 OY 4693 ATCAGAGGCCCTATATGAACTTTATACGTAGCTATATCTATATATATTAATTCTGTACAT 4752
 Db 480 atcagaagccctaataagaacttatacagtgtagctatatacataataaattctgtaacat 539
 OY 4753 AGCCATATTTTACAGTAAATGTAAGCTGTATTTTATATTTTAAATTAACACAGTGGCT 4812
 Db 540 agccataatttacaagtgaaatgtaagctgttattatattataaataaagcacgtgct 599
 OY 4813 AAAAAAA 4819
 Db 600 aataaca 606
 RESULT 11
 PCT-US02-07787-35
 Sequence 35, Application PC/TUS0207787
 GENERAL INFORMATION:
 APPLICANT: The Brigham and Women's Hospital, Inc.
 APPLICANT: Yates, Karen
 APPLICANT: Mizuno, Shuichi
 APPLICANT: Glowacki, Julie
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SKELETAL DEGENERATION CONDITIONS
 FILE REFERENCE: BO801/7244/AA/REP
 CURRENT APPLICATION NUMBER: PCT/US02/07787
 CURRENT FILING DATE: 2002-03-12
 PRIOR APPLICATION NUMBER: US 60/274,980
 PRIOR FILING DATE: 2001-03-12
 NUMBER OF SEQ ID NOS: 79
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 35
 LENGTH: 5011

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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-07787-35

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Query Match	10.5%;	Score 511.2;	DB 1;	Length 5011;
Best Local Similarity	52.5%;	Pred. No. 1.4e-88;		
Matches 1367;	Conservative	0;	Mismatches 1178;	Indels 59; Gaps 9;

OY	1811	CATTCACCTGGGGCCACCGCTTACGAGAGACACGACAGATGATCTGGAACTT	1870
Db	2143	cacatlcacttggcca--ggagcgacctcccaaccgtaatgtaacacttccatc	2200
OY	1871	CAAAAGGGTAAATCGTTGGAAATCTCGCGACAGTGTGGGAAGTGGAAAAACCTCTCATTT	1930
Db	2201	ccgaaagtgcttcttgtagccgtagtggcgaagtgaggctcgtggaagtcgtccctctc	2260
OY	1931	TCAGCCATTTTTAGCCAGATGACGCTTCTTAGAGGGCAGCATTTGCATTCAGTGAACCTTC	1990
Db	2261	tcagccctcttgctgagatgtagtgaacaagtgaggggggcaacgtgctatcaagggctcgtg	2320
OY	1991	GCTTATGTGGCCAGACGAGCGCTGGATCCATCGCATCGCTAGAGAGCAACACTCTGTTT	2050
Db	2321	gctcatgtgcccagaagagcgcttgatctcagaatgatctctccggaataacatcccttct	2380
OY	2051	GGGAAGAAATATGATGAAGAAAGATCAACTCTGTGCTGACACGCTGCTGCCTAGAGGCTT	2110
Db	2381	ggatgtgaagcttgtaggaatacataatacagttccgtatagaagcgcttgyccctcccca	2440
OY	2111	GACCTGSCCATTTCTTCCACAGCAGCATCGACGAGATTTGAGAGCGAGGCCAACCTG	2170
Db	2441	gacctggaatactcgtcccagtgggatctgacagagatgtgcgaagaaggcgtagaactg	2500
OY	2171	AGGGGTGGGGCGCCAGAGAGATCACCTTGCCCGGGCCCTTTATAGAGAGAGACATC	2230
Db	2501	tcgtggggccagaagacagcgctgtagcgccggccggcgctgtactccaacgctgaacat	2560
OY	2231	TACATCTCTGGACGACCCCTCAGTGCCTTAGATGCCCATGTGGCMAACACATCTTCAT	2290
Db	2561	tacctcttgatgatccctctcagtagagtgatgccatgtgggaataacacatcttgaa	2620
OY	2291	AGTGTCTT-----CCGGAACATCTCAAGTCCAGACAGTTCCTGTTTGTATCCACCAG	2344
Db	2621	aatgtgatgcccccaaggagtagctgtaagaacaagacagcgatcttgtatcgacagcg	2680
OY	2345	TTACAGTACCGGTTGATCTGTGATGAAGATCTTCATTAAGAAAGGCGTGATTAACGAA	2404
Db	2681	atgagcttacttgcgcgcaggttgagcgtcaatcactgtaatgtagtgcgcaagaatctctgag	2740
OY	2405	AGAGGACCCATGAGAACTGATGAATTTAAATGGTGAATGATGCATTCACATTTTAAATAAC	2464
Db	2741	atggtgctcttaccagagcgctgctgtctgtagaagcgccctcgtcgtatcttcigtatcc	2800
OY	2465	CTGTTGCTGGGAGACACCGCCAGTT---GAGATCAATTCAAAAAGGAAACCAAGTGT	2521
Db	2801	tatgcagacaagcgacagagcagagatgcaagagaaacgggtgtcaagcgctcagcgt	2860
OY	2522	TCACAGAAGAAAGTCCACAGACAGAG-----GTCTTAAACAGAGATCATTAAAGAAG	2573
Db	2861	ccagtggaaggaagaaagacaaatggaagaaatgagcatgctgtgtgacggaacagtgcaggaag	2920
OY	2574	AAAAAGCAGTAAAGCCAGAGAGAGGGCAGCTGTGTGCAGCTG-----	2615
Db	2921	caactgacagagacagctcagcagctctctctctctatagtgggagacatacgaagcaaac	2980
OY	2616	AAGGAAAGGGCAGGCTTCAGTGCCTGTGTCAGATATATGTTGTACATCCAGGCTGCTG	2675
Db	2981	aacagcaacggaagatcgtcagaagaagcttgaggccaagaagaaagagacacttgaaactgtg	3040
OY	2676	GGGGC-----CCCTTGGCATTCCTGTTATTTATGCGCCCTTTTATGCTCTGAATGTAGCC	2728
Db	3041	gagcgcttacaagggcagacaagggcggtcaagcttccgtgtactcgtgtaactgaatgaag	3100

QY	1931	TCAGCATT	TGAGCCAGATGACGCTTCT	TGAGGGCAGCATTTGCAATCAGTGAAC	CTTC	1990	
Db	2261	TCAGC	ccctctctg	ctctgagatggaacaa	gtgagagcaacgctg	ctcagagctcgtg	
QY	1991	GCTTATG	GGCCCGACGAGGCTGGATCC	TCAATGACACTGAGAGCAACATCCTG	TTT	2050	
Db	2321	g	ccatctgtgc	acacagcagcgcctg	gattcagaa	gattcctcccgaa	
QY	2051	GGGAA	GAAATATGATGAAAGAA	ANTACACTCTGTCTCTACAGCGCTCGCTGAGG	CTT	2110	
Db	2381	g	gattc	gacgctg	cagctg	gagagacatat	
QY	2111	GACCTG	GGCATTCTTCCACAGCAGCTC	AGCGAGATTTGAGAGCGAGACCAAC	CTG	2170	
Db	2441	g	acctgtg	aaatcctgtccca	gtgagatcg	gacagaa	
QY	2171	AGCGT	GGGCGCCCGACGAGATCAG	CGTTGCCGGGCGCTGTATATGATACAGGAG	CACT	2230	
Db	2501	ct	gtggg	gccaagacgcgcgt	gtgacccgtg	cccggtgtg	
QY	2231	TGACAT	CTGAGCAGCCCCCTCAGTGG	CTTATAGATGCCATATGTGGGCAACACATCTT	CAAT	2290	
Db	2561	t	acctcttc	gatgatccccctc	tcagcagtgatg	cccatgtg	
QY	2291	AGTGTAT	-----CGGAA	CACTCTCAAGTCCAGACAGTTCTGTTT	GTATACCCACAG	2344	
Db	2621	a	atgtgtat	gtgcccccaagggagatc	gtgaaacaa	gcgagatctgtgtc	
QY	2345	TTACAGTAC	CGGTGTGATCTGTATGAA	AGANTTCTATCAAAAGGGCGTCTTAC	GGAA	2404	
Db	2661	at	gagc	tactctgtccgcgcggtgtg	agcgtc	atcatatg	
QY	2405	AGAGCA	CCACCATGAGAACTGATGA	ATTTAAATGTGATACATACATTTT	TAATAC	2464	
Db	2741	a	tgggc	ctctacacagagcgtcgtgc	tcgagacg	gcttcg	
QY	2465	CTGTTC	GCGSAGAGACCCGCAAT	TT-----GAGATCA	ATTTCAAAAAGGAACAGTGT	2521	
Db	2801	t	atgtcc	agcagcagcagcagcagc	atgtgaa	gagaa	
QY	2521	TCACAGA	GAAGATGCACAAAGCAAG	-----GTCTTAAACAGS	ATCAATTAAGAAG	2573	
Db	2861	cc	aggaaggaaggaagga	aaagcaatg	ggagaa	tgtgc	
QY	2574	AAAAAG	CAATAAAGCCAGAGAA	GGGACAGCTTGTGCAGCTG	-----	2615	
Db	2921	ca	actgtg	agagacagcgtcagc	agctctc	ctc	
QY	2616	AAGGAA	AGGGCAGGTTCAAGTCC	CTGCTCAGATATGTGTCAATC	CAGCTGTG	2675	
Db	2981	a	acagc	acccgacgaagatctg	caagaagctgtg	gccaaga	
QY	2676	GGGGC	-----CCCTTGG	CATCTCTGTTATATG	GGCCCTTTTATGCTGA	TATAGCC	2728
Db	3041	g	agagc	gtacaa	ggtgcagaa	gagcaggtc	
QY	2729	AGCAGC	CCCCCTTACAGACACTG	TGTTAGATTACTGATCAAC	GAAAGGCGGAAAC	2788	
Db	3101	g	acctgtg	actcttcaatctc	ctcc	tcagacatctc	
QY	2789	ACTGTG	ACT-----CGAGG	AAAGAGACCTCGGTGAGT	GACAGCATGAGAGCA	TAATCTT	2842
Db	3161	g	gcgtgt	cttccaacat	tattgtc	cagcgtc	
QY	2843	CATATG	AGATCTATGCGACATCT	AGCCCTCTCATG	GGCAGTATGCTGTAT	CTGTAA	2902
Db	3221	ca	gagag	acacagaa	gtccgtg	acgtctatg	
QY	2903	GCAAT	TGAGAG-----AGT	TGCTTGTGCAAGGGG	ACAGCTCGAGCTCTCC	CGCGTG	2956
Db	3281	g	cgctgt	ttgtgtc	actctc	atc	
QY	2957	CATGAC	GAGCTTTCCGAAGATC	CTTTCGAAGCCCTAT	TAATATTTTTCAGCA	AGACCC	3046

Db	3341	cacgtgaaacctgctgcacaaacatctctgaggctcaaccatgaagctctctttagcggaaaccc	3400
Oy	3017	ACAGGAGGAGATTCACACAGAGTTTTCACAAAGACATGATGAAGTTGACGTGGCGTCGG	3076
Db	3401	agtgggaacctgtgtgaaacgctctctccaaaggatcggaaacagctggaatccatgctccg	3466
Oy	3077	TTCCAGGCGCAGATGTTTCATCCAGAAAGTTATCTCGTGTCTGTGTCGGAAATGATC	3136
Db	3461	gagtgatacaagatggttccatctgagctctccctgttcaacgtcattgtgtgcgcatagttacc	3520
Oy	3137	GCAGGAGCTCTTCCCGTGGTCTTGTGTGGCAGTGGGCCCCCTTGTCATCTCTTTACAGTC	3196
Db	3521	ctgtgtgccaagcccaatcgccgcatacatcatccgccctgtgcctcaactactcttc	3580
Oy	3197	CTGGACATTTGTCCTCCAGGTCGTGATTGGGAGCATCAACGTCGTGGACATATCAACGAG	3256
Db	3581	gtccaaagagttctaaagtgtgtctctcccgcaagctgaaagcctccgaagtcggtcaagccg	3640
Oy	3257	TCACCTTTCCTCTCCCATCCAGTCCAGATACAGAGGCGCTTGGCCACATCCACGCTTAC	3318
Db	3641	tcoccggtctattcccatctcaacggaacctgtctggggctcaagcgtcatctcgagcttc	3700
Oy	3317	AATATAAGGACGAGATTCTTGCCACAGATACAGAGAGCTCTGTGGATGACACCAAGCTCTCT	3376
Db	3701	gaagaaagcagaagcgtcttcaatccacagagtgatgactgaaagtgtgacgaagaccagaagcgc	3760
Oy	3377	TTTTTTTTTTGTTTACGTGTGGATGGGATGGGTCGGTGTGGGCTGGACCTCATACGATAC	3436
Db	3761	tattaccccacgaatcgtgtgcacaagaagtgtggtccggtgagagtgatgtgtgtggacac	3820
Oy	3437	GCCCTCATACACACACAGGGGCTGATGATGCTTATGTCACAGGGCAGATTCCCCACGCC	3496
Db	3821	tgaatcgctctgtgtgtgtgcctgt	3880
Oy	3497	TATCGGGCTCTCGCCATCTTTATGCTGTCCAGTTAACGGGCGTGTCCAGTTTACGGTC	3556
Db	3881	tgt	3940
Oy	3557	AGACTGGCATCTGTGACAGACAAAGCTGCATTCACCTCGTGTGGAGGATTCATCATCATATTT	3618
Db	3941	cgaatgtcatcatctgaataaggaaacacaatcgtgtgcggtgtgaaaggtctcaaggatattca	4000
Oy	3617	AAGACTCTGTCTTGTGGAAGCACTGCGCAGATTTAAACAAAGCTCCCTCCCTACATCG	3676
Db	4001	gagactgtagaa---ggaaggtccctgtgcaaatccgaatccgaagctccgcgccgaagcgtcg	4056
Oy	3677	CCCCAGAGGAGAGGTGACCTTTTGAAGACGCAGAGATGAGTACCGAGAAAACTCCCT	3736
Db	4058	cccccaagtgtggtgcgaagtgtatctcggaactactgtcgtgtacacgaagaaacctgac	4117
Oy	3737	CTCTGCTTAAGAAAGTATCTCTTCACGATCCAAACCTTAAGAGAAAGATTGGCTTGTGGG	3796
Db	4118	tctgtctctcagccacatcaatgtcatcatcaatctgaatgtgggaagaaagtcgtgcatctgtggg	4177
Oy	3797	CGGACAGATACAGGAAGTCTCGTGTGGGAGTGGGCCCTTTCGTCGTGGTGGAGTTATCT	3856
Db	4178	cggagcgggaagctgtggaagtcgtccctcggaacctgtgctattctcgatcaaaagagtcgtcc	4237
Oy	3857	GGAGGCTGATCAAGATTGATGGAGTGAAGATCAGTATTTGGCTTTGGCCAGCTCCGA	3916
Db	4238	gaaggaagatcatcatcatcgtgtgtcatcaaatcgcgaagaatcgtgctgtcgaagactccgc	4297
Oy	3917	AGCAAACTCTCTATCATTTCTCTCAAGACCGGTCGTCTTGTAGTGCACATGTACAGATCAAT	3976
Db	4298	tctcaagatcaatcaatccccccaggaacctgttctgttcttggtgttccctccgaatgaac	4357
Oy	3977	TTGGAACCCCTTCAACCGATCAGTACATGAAGACAGATTTTGGATGGCCCTGAGAGGACAC	4036
Db	4358	ctggaaacctatccagcaagatctcgtgtgtgaagaagctctgtgagctccctgtgagctgtgccac	4417
Oy	4037	ATGAAACAATGTATTGTGCTACGTTACTCTGAAACTTGAATTCGAAGTATGGAGATGGG	4096

Db 4418 ctgaaggaactcgtcgaacccctccctgaacagctagaccatgatgtgcagaagggcgg 4477
QY 4097 GATTACTTCTCAGTGGGGGAAAGGAGCTCTTGTCATAGCTAGACCCCTGCTCCGCCAC 4156
Db 4478 gagaacctgaatgtcgggaagcgcacagctgtgtctcagcccgccctgtggaag 4537
QY 4157 TGTAGATTCTGATTTTGTAGTGAAGCAGACGCTGCATGACACAGAGACACTTATG 4216
Db 4538 aagaagatccctgtgtgtgtagaagcgcagcgcgtggaacctgaaacggaacctc 4597
QY 4217 ATTCAAGAGACCATCCGAGAGCATTTTGACACTGTACCATCTGACCATCCCATGCG 4276
Db 4598 atccagtcacccatccgcagacagctcgaagctgacagctccctaccatgcgccacgg 4657
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Db 4658 ctcaacacatcaatgagctacaagaagtgatcgtcttgagaaagggagaatccagag 4717
QY 4337 TTTGACACCCCATCGTCTCTCTG 4360
Db 4718 taaggcgcccatcgagacctctg 4741

RESULT 13
US-09-930-213-287
Sequence 287, Application US/09930213
GENERAL INFORMATION:
APPLICANT: ROSENTHAL, ANDRE
APPLICANT: HINZMANN, BERND
APPLICANT: SCHAEFER, REINHARD
APPLICANT: ZUBER, JOHANNES
APPLICANT: TCHE-NITSE, OLEG
APPLICANT: GRIPS, MARTIN
APPLICANT: HELNEGEL, MARTIN
APPLICANT: SCHMITZ, ANNE-CHANTAL
APPLICANT: SEBS, CHRISTINE
TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
FILE REFERENCE: ALBRE-14
CURRENT APPLICATION NUMBER: US/09/930, 213
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: DE 10004102.7
NUMBER OF SEQ ID NOS: 885
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 287
LENGTH: 4231
TYPE: DNA
ORGANISM: Homo sapiens
US-09-930-213-287

Query Match 9.0%; Score 437.4; DB 5; Length 4231;
Best Local Similarity 48.8%; Pred. No. 2e-74;
Matches 1244; Conservative 0; Mismatches 1296; Indels 9; Gaps 2;

QY 1844 AACTGACACATCATGATCTGAGATCCAGAGGGTAAGTGAATCGGCGAGT 1903
Db 1394 acttaaaagcccttcccttaacgtacgacctgycgaattgttaagctgtgtgccc 1453
QY 1904 GTGGGAAGTGAAGAAACCTCTCTCATTTTCAAGCCATTTTGAAGCAGATGACCTTCTAG 1963
Db 1454 gtgggaacaggaagatcactcgttaagtgcgtgcggggaattgcccccaagtcac 1513
QY 1964 GGCGAGATTGCAATCAGTGAAGAACTTCGCTTATGTGGCCGACGAGCTGTGATCTCAT 2023
Db 1514 gggctgtgcagcgtgcataggaattgctcctatgtctcagcagccctgggtctcgc 1573
QY 2024 GCTACTGTGAGAGACAATCTGTTGGGAAGAAATGATGAAGAATTAACAACCT 2083
Db 1574 ggaactctgaggaataattatttttgggaagaataatgaagaagcagcatalgaaaa 1633
QY 2084 GTGCTGAACAGCTGCTGAGGCTGAGGCTGACCTGGCCATTTCTCCAGCAGGACCTGACG 2143

Db 1634 gtcataaagctgtgtccttgaaaaagattacagctgtttggagatgtgtatcgtact 1693
QY 2144 GAGATTGAGAGCAGAGACCAACTGAGCGGTGGGACAGCGGAGATGACGCTTGGC 2203
Db 1694 gtgataagatcgcgggaacccaacgctgagtgagcagaagaacgaggttaaccttgca 1753
QY 2204 CGGGCTTGTATAGTGAAGACGACATCTATCTGTGAGACGACCCCTGCTGACTTAA 2263
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QY 2264 GCCCATGTGAGCAACACATCTTCAATAGCTATCCGGAACATCTCAAGTCCAGACA 2323
Db 1814 ggggaagtgtaagaagacactgttgcaacgtgtatlttgcaatttgtaagaagatc 1873
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Db 1874 acaatttgatcatcatcagctgcagtcacccaagctgcgaagtcagttctgtatgt 1933
QY 2384 AAGAGGGCTGTATTACGGAAGAGACCCCATGAGGAACTGATGATTTAAATGTTGAC 2443
Db 1934 aaagatgtaaaaatgttgagaagggacttaacactgattcttaaatctgtatagat 1993
QY 2444 TATGCTACATTTTAAATTAACCTGTTGCTGGAGAGACACCGCATTTGATGATCAATCA 2503
Db 1994 ttgtgctccctttaaagaagataatgaggaagtgaacaacctccagttccaggaact 2053
QY 2504 AAAAAGAAACCATGTGTTTACAGAGAAATGACAGAAAGGTTCTTAAACAGATCA 2563
Db 2054 ccacacataaggaatcgtacccttcgaaggtctcglttgtctcaacaactctctaga 2113
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Db 2354 gtaactgttaaatgaggaagaaatgttaaccggaagctagatcctaactgtactaga 2413
QY 2864 ATCTAGCCCTCTCTCATGAGCATGCTGATGCTGAAAGCCATTCGAGAGAGTGTCTTT 2923
Db 2414 atttaaatgtttaaactgtacgtcgttcttcttgcatagaagaatctctatgtta 2473
QY 2924 GTCAAGGGCAGCGTGCAGCTTCTCCCGGCTGATGAGAGCTTTTCCAGAGATCTCT 2983
Db 2474 ttctacgtccttgttaactccttcaacaacttgcacaacaaatgttggatcaattctg 2533
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Db 2534 aaagctcgtgatatcttcttgatagaatccaatagaagaatlttaaatcgttctccc 2593
QY 3044 AAAGCATGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3103
Db 2594 aaagacattgacacattgagatltgtgcgcgtgacgttlltagatltcatcagaca 2653
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Db 2654 ttgtcaagaagtgatgt 2713
QY 3164 GCAGTGGGCCCCCTTGTGATCTCTTTCATGCTGATGATGATGATGATGATGATGATGAT 3223
Db 2714 ccttgtgtcccttgagatcaatttcttcttcttggtgagatatttlttgaaacgtca 2773

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OY 3224 CGGAGCTGAAGCGTCTGCAATATATCAGCGATGACCTTTCTCTCCACATCAGCGCC 3283
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Db 2774 aagagatgtgaagcgccggaatctacaactcgcgagtgccagtgttctccacttgcattc 2833
OY 3284 AGCATACAGGCGCTTGCCACCATCCAGCGCTACAAATAAGGGCAGAGATTCTTCACAGA 3343
    || || || || || || || || || || || || || || || || || || || || || ||
Db 2834 tctctcaggggctctgagaccatccggcatatacaagaagagaggtgtgcaggaactg 2893
OY 3344 TACCAGAGCTGCTGGATGACCAACCAAGCTCTTTTGTGTAGCTGTGCGCATGCGG 3403
    || || || || || || || || || || || || || || || || || || || || || ||
Db 2894 ttgatgtcacacccaggtattacattcagaggtctgttctgttcttgacagctccgc 2953
OY 3404 TGGGTGCTGTGCGCTGAGACCTCATCAGCATGCGCTCCCTCACACACAGGGGCTGATG 3463
    || || || || || || || || || || || || || || || || || || || || || ||
Db 2954 tgggtgcgctcgcgtcgagatgcacatctgtgcacatctgttgcacatccgttgccttgg 3013
OY 3464 ATCGTCTTATGCAAGGGGAGATTCCCGCAGCCATGCGGGCTCGCCATCTTATGCT 3523
    || || || || || || || || || || || || || || || || || || || || || ||
Db 3014 tccctgttcttgcacaaaactctgagtcgcgaggttggtttggcactgtctatggcc 3073
OY 3524 GTCCAGTTAAGCGGGCTGTTCCAGTTTACGGTCAAGCTGCGATGTGACACAGAACTCGA 3583
    || || || || || || || || || || || || || || || || || || || || || ||
Db 3074 ctcaagctcatg99gatgttgcagtggtgtgtcgcacaaagtgtgaagtgtgaatatg 3133
OY 3584 TTCACCTCGGAGAGGAGATCAATCACTACATTAAGACTCTGCTCTGGAAAGCACTGCC 3643
    || || || || || || || || || || || || || || || || || || || || || ||
Db 3134 atgattccagtaagaaggtccatltgaatcacagacctt-----gaaaagaagacct 3187
OY 3644 AGAATTAAAGAAAGGCTCCCTCCCTGACTGCGCCAGAGAGGAGAGTGAACCTTTGAG 3703
    || || || || || || || || || || || || || || || || || || || || || ||
Db 3188 ttggaataatcagaagaagcccaacccagcgcgtcccatgaagaagtataatcttggac 3247
OY 3704 AACCGACAGATGAGCTACCGAAGAAACCTCCTCTGCTCTAAAGAAATATCTTCAAG 3763
    || || || || || || || || || || || || || || || || || || || || || ||
Db 3248 aatgtgaactcatgtacagtlccagtggtgcctctgttactgaagcatctgcagcagctc 3307
OY 3764 ATCAAACCTTAAAGAGGATTTGGATTTGGGGGCGAGACAGGAAATCCTCGCTG 3823
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Db 3308 attaaatacaagaagaaggttgcattgtggaagaacccgagctgtgaaaaagttccctc 3367
OY 3824 GGGATGCGCCCTTCCCTGCTGCTGAGATTATCTGAGGCTCATCAAGATTTGATGAGTG 3883
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Db 3368 atccagcccttlttaattgtcaga---accggaagttaaatlttgatgtataagatc 3424
OY 3884 AGAATCAATGATTTGGCTTGGCCGACTCCGAAACAACTCTGTATCTTCTCAAGAG 3943
    || || || || || || || || || || || || || || || || || || || || || ||
Db 3425 ttgacaactgaatltgacatccagatlttaagagaagaatgtcaatcatcaccagaa 3484
OY 3944 CCGGTGCTGTTCACTGCGCACTGTAGATCAAAATTTGGACCCCTTCAACCACTGAA 4003
    || || || || || || || || || || || || || || || || || || || || || ||
Db 3485 ccgttlttltgacttgaacaatltgaagaacacgtgtatcccttlaaggaacaaagat 3544
OY 4004 GACGAGATTTGGAGTCCCTGAGAGAGACACATGAAAGATGATTTGCTCAGCTACCT 4063
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Db 3545 gaggaactgtggaatgtccttaacaagagtataactttaaagaacacatltgaagatcctc 3604
OY 4064 CTGAACCTTGAAATCTGAGTGAGTGAAGATGGAATCTTCAAGTGGGGAACGGCAG 4123
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Db 3605 ggtlaaaatgtactagtaattagcagaatcagaatccaaatttagtltgtgcaagaagcaa 3664
OY 4124 CTCTTGTGCAATAGTAGAGCCCTGCTCCGCCACTGTAAGATTTGATTTTGAAGAGCC 4183
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OY 4184 ACAGCTCCATGAGACAGAGACAGACTTATGATTAAGAGACATTCGAGAGCAATTT 4243
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Db 3725 accgcaaatgtggaatccaaagaactgtagttaatacaaaaaadlcccggaagaatltt 3784
OY 4244 GCAGACTGTACATGCTGACCATTTGCCCATGCTGCAACAGGTTTCTAGGCTCCGATAGG 4303
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Db 3905 aataagagagcattatlttaacaagtgtg 3933

RESULT 14
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: Sequence 1, Application US/09647140A
: GENERAL INFORMATION:
: APPLICANT: Fox Chase Cancer Center
: APPLICANT: Krush, Gary D.
: APPLICANT: Lee, Kun
: APPLICANT: Belinsky, Martin G.
: APPLICANT: Bain, Lisa J.
: TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
: TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
: FILE REFERENCE: PCCC 98-02
: CURRENT APPLICATION NUMBER: US/09/647,140A
: CURRENT FILING DATE: 2001-05-21
: PRIOR APPLICATION NUMBER: PCT/US99/06644
: PRIOR FILING DATE: 1999-03-26
: PRIOR APPLICATION NUMBER: 60/079,759
: PRIOR FILING DATE: 1998-03-27
: PRIOR APPLICATION NUMBER: 60/095,153
: PRIOR FILING DATE: 1998-08-03
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 4231
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-647-140A-1

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Best Local Similarity 48.88; Pred. No. 2e-74;
Matches 1244; Conservative 0; Mismatches 1296; Indels 9; Gaps 2;

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Db 1394 actctacaaggcccttcccttactgtcagacctggcgagatgttagctgtgcggccc 1453
OY 1904 GTGGGAAGTGGAAAAACCTCTCTCATTTTCAGCAATTTTAGGCCAGATGACGCTTTAGAG 1963
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Db 1634 gtctaaagagcttgtccttgaaaaaagatttaacagctgttggaggtatgtgatctgact 1693
OY 2144 GAGATTTGAGAGCGACGACGACCAACCTTGAGCGGTGGCAGCGCCACAGAGATCACTTCCC 2203
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Db 1694 gtgatatgagatcgggggaacacgcgtgagtgagggcagaagaagcaggttaaaccttgca 1753
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; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Dickson, Mark C.
; APPLICANT: Jones, Lee W.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 780CIP
; CURRENT APPLICATION NUMBER: US/10/011,154
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/524,038
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/404,284
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 4670
; SOFTWARE: HY-patent.pl Version 3.1
; SEQ ID NO 3846
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-011-154-3846

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Query Match      8.5%; Score 409.8; DB 7; Length 426;
Best Local Similarity 99.5%; Pred. No. 2,9e-69;
Matches 411; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 134 atgacacagagagacagactattgatccaagagacatccgagagacatttcagactgt 193
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QY 4253 ACCATGCTGACATTCGCCATCGCCTGCACACAGGTTCTAGGCTCCGATAGGATTTATG 4312
    |||||||
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    |||||||
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QY 4433 CTCCTGTTGACGAGTCTCTTTCTTTTACAGCATTCGCAATTCCTGCTGGG 4485
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Db 374 ctccctgtgacagagctctcttctttagagcatgccaatccctgctgtgg 426
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Search completed: August 11, 2002, 11:11:20
Job time: 6765 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 11, 2002, 09:20:05 ; Search time 25.86 Seconds

(without alignments)
1357.292 Million cell updates/sec

Title: US-09-528-031-2

Perfect score: 7308

Sequence: 1 MKDIDGKEYITPSGYRSV.....DSRPYAMFAAEKVAVKG 1437

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents-AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7308	100.0	1437	3	US-09-061-400-2
2	7298	99.9	1453	2	US-09-001-273-2
3	7298	99.9	1453	4	US-08-843-459A-2
4	2082	28.5	1531	1	US-08-463-092B-4
5	2082	28.5	1531	2	US-08-462-109A-4
6	2082	28.5	1531	2	US-08-460-907B-4
7	2082	28.5	1531	3	US-08-463-179A-4
8	2082	28.5	1531	3	US-08-461-384B-4
9	2075	28.4	1531	1	US-08-141-893-2
10	2075	28.4	1531	1	US-08-463-092B-2
11	2075	28.4	1531	2	US-08-462-109A-2
12	2075	28.4	1531	2	US-08-460-907B-2
13	2075	28.4	1531	3	US-08-463-179A-2
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18	2055.5	28.1	1528	2	US-08-460-907B-6
19	2055.5	28.1	1528	3	US-08-463-179A-6
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21	2013.5	27.6	1622	4	US-08-972-927-6
22	2006	27.4	1261	4	US-09-439-313-538
23	1991	27.2	1621	4	US-08-972-927-3
24	1894.5	25.9	1328	4	US-09-439-313-537
25	1759	24.1	1581	4	US-08-726-320-3
26	1759	24.1	1581	4	US-09-208-716-3
27	1757.5	24.0	1580	4	US-08-726-320-1

28	1757.5	24.0	1580	4	US-09-208-716-1	Sequence 1, App11
29	1732	23.7	1581	4	US-08-726-320-4	Sequence 4, App11
30	1732	23.7	1581	4	US-09-208-716-4	Sequence 4, App11
31	1730	23.7	1477	3	US-08-492-459-10	Sequence 10, App1
32	1730	23.7	1477	3	US-08-423-752-10	Sequence 10, App1
33	1730	23.7	1477	3	US-08-945-994-3	Sequence 3, App11
34	1730	23.7	1477	4	US-08-716-873-24	Sequence 24, App1
35	1730	23.7	1477	4	US-09-368-431-24	Sequence 24, App1
36	1730	23.7	1477	4	US-09-414-006-10	Sequence 10, App1
37	1669.5	22.8	1581	2	US-08-404-531B-6	Sequence 6, App11
38	1669.5	22.8	1581	3	US-08-476-900A-6	Sequence 6, App11
39	1669.5	22.8	1581	3	US-08-488-546A-6	Sequence 6, App11
40	1669.5	22.8	1582	2	US-08-404-531B-9	Sequence 9, App11
41	1669.5	22.8	1582	3	US-08-476-900A-9	Sequence 9, App11
42	1669.5	22.8	1582	3	US-08-488-546A-9	Sequence 9, App11
43	1669.5	22.8	1582	4	US-08-726-320-5	Sequence 5, App11
44	1669.5	22.8	1582	4	US-09-208-716-5	Sequence 5, App11
45	1528.5	20.9	1498	2	US-08-404-531B-28	Sequence 28, App1

ALIGNMENTS

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RESULT 1
US-09-061-400-2
; Sequence 2, Application US/09061400
; Patent No. 6077936
;
GENERAL INFORMATION:
; APPLICANT: SHYUAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; NUMBER OF INVENTIONS: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,400
; FILING DATE: 16-APRIL-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-061-400-2
;
Query Match 100.0%; Score 7308; DB 3; Length 1437;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MKDIDGKEYITPSGYRSVRSCTGRDDEDSKFRTRPLECODEATAETAAAGGS 60
DB 1 MKDIDGKEYITPSGYRSVRSCTGRDDEDSKFRTRPLECODEATAETAAAGGS 60
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Db 241 ALNRYGVRLRGAILTMAKKTILKLNKEKSLGELINCSNDGOMFPAAVGSLIAG 300
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Db 301 PVVALIGMIYNYIILGPTFLGSAVFLFYPAMMFASRLTAFRRCKVATDERQKME 360
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Db 361 VLTYYIKFKIMYAMVAFKFSQVOKIREERRILEKAGYFOSITVGVAPYVVIASVYTF 420
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Db 481 NKPSAPHIKIEKKNATLMDSSHSIONSPKLTPEMKDKKASRCKKEVROLOTEHQA 540
Qy 541 VLAEOKGLLDDSDRPSPEEERKHILGHLRLOTLHSIDLEIOEKLVGICGSVSG 600
Db 541 VLAEOKGLLDDSDRPSPEEERKHILGHLRLOTLHSIDLEIOEKLVGICGSVSG 600
Qy 601 KTSLSIALGQMTLEGGSLAISGTPAYAAQAMILNATLRDNIIFGKEYDEERYNSVNS 660
Db 601 KTSLSIALGQMTLEGGSLAISGTPAYAAQAMILNATLRDNIIFGKEYDEERYNSVNS 660
Qy 661 CCLRPDLALPSSDLTEIGERGANLSSGOROISLARALYSRSTYIILDDPLSALDAV 720
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Db 781 FNNLLGTPVEINSKKETSGSOKSODKPKTGSIKKEKAVKPEEQOLVLEEKGGGS 840
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Db 961 KFPPTTPTGRILNFSKDMDEVDRLPPOAMFTQNVILVEFCVMAGVPMFLVAVGP 1020
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Db 1021 LVILFSLVLIYSRVLIRELRKLDNITOSPFLSHITSSIOGATITHAANKGEFLHARQEL 1080
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Qy 1141 GLFOFTVRLASETEARTSVERRINHYIKTSLSEAPARIKKNKAPSPDMPOGEVTFENAM 1200

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Db 1141 GLFOFTVRLASETEARTSVERRINHYIKTSLSEAPARIKKNKAPSPDMPOGEVTFENAM 1200
Qy 1201 RRENPLVLKKSFTFKREKIGIVRTGSGKSSIGMALFLRYVELSGCCICIDGVRID 1260
Db 1201 RRENPLVLKKSFTFKREKIGIVRTGSGKSSIGMALFLRYVELSGCCICIDGVRID 1260
Qy 1261 IGLADRSKLSIIPQEPVLFSGTVRSNLDPEFNOYTEDOIMDLERTHMECTAOLPLKLE 1320
Db 1261 IGLADRSKLSIIPQEPVLFSGTVRSNLDPEFNOYTEDOIMDLERTHMECTAOLPLKLE 1320
Qy 1321 SEVMGNDNFVSGEROLICARALLRHCKILLIDETAAMDTEIDLIOETIREAFADCT 1380
Db 1321 SEVMGNDNFVSGEROLICARALLRHCKILLIDETAAMDTEIDLIOETIREAFADCT 1380
Qy 1381 MFTIARHLTVGSDRIWLAOGOVEFPTSVLLSNDSRFRYAMFAAENKVAVKG 1437
Db 1381 MFTIARHLTVGSDRIWLAOGOVEFPTSVLLSNDSRFRYAMFAAENKVAVKG 1437

RESULT 2
US-09-001-273-2
; Sequence 2, Application US/09001273
; Patent No. 5994130
; GENERAL INFORMATION:
; APPLICANT: SHYIAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,273
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON, Gillian M
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: MTL-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1453 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-001-273-2

Query Match 99.9%; Score 7298; DB 2; Length 1453;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 197 LSTVCLMINTQLAGFSGPAFAVVKHLEETQATBSNLOYSLLVGLLTELIVRSMSLALTW 256
QY 241 ALMYRTGVRLRGAILTMAFAFKILTKNIKESIGELINICSNQGMHFEAAAGSLIAG 300
Db 257 ALMYRTGVRLRGAILTMAFAFKILTKNIKESIGELINICSNQGMHFEAAAGSLIAG 316
QY 301 PVVAIIGMTIYNYIILGPTGLSAGEVILEFYPAMMFASRLTAYFRRCVATDERVOKME 360
Db 317 PVVAIIGMTIYNYIILGPTGLSAGEVILEFYPAMMFASRLTAYFRRCVATDERVOKME 376
QY 361 VLTIFYIKMYAMVAKAFSOSVOKIREBERRILEKAGYPOSITVGVAVIVVIVASVTFESV 420
Db 377 VLTIFYIKMYAMVAKAFSOSVOKIREBERRILEKAGYPOSITVGVAVIVVIVASVTFESV 436
QY 421 HMTLGFDLTAAQAFVTVYVENSMTFALKVTPESVKSLSSEASVAVDRKSLFLEEVHMIK 480
Db 437 HMTLGFDLTAAQAFVTVYVENSMTFALKVTPESVKSLSSEASVAVDRKSLFLEEVHMIK 496
QY 481 NKRPASPHIKIEMKNATLANDSSHSSIONSPLTPKMKKDKRASRGKKEKVRQLOREHQA 540
Db 497 NKRPASPHIKIEMKNATLANDSSHSSIONSPLTPKMKKDKRASRGKKEKVRQLOREHQA 556
QY 541 VLAEOGHLILDSDERPSPREEEGKHILHGLRLQRTLSHIDLEIOBKLVIGCSVSG 600
Db 557 VLAEOGHLILDSDERPSPREEEGKHILHGLRLQRTLSHIDLEIOBKLVIGCSVSG 616
QY 601 KTSLSAILGOMTLEGSAISGTFPAVVAQOAMILNATLBNLTLPCKEYDEERYNSVLS 660
Db 617 KTSLSAILGOMTLEGSAISGTFPAVVAQOAMILNATLBNLTLPCKEYDEERYNSVLS 676
QY 661 CCLRPLDALIPSSDLTEIGERGANLSGGORISLARALYSDRSIYLLDPLSALDAHVG 720
Db 677 CCLRPLDALIPSSDLTEIGERGANLSGGORISLARALYSDRSIYLLDPLSALDAHVG 736
QY 721 NHIFNSAIRKHLKSKTVLFTYHOLQYLVDCEYIFMKEGCITRGHEELMANGDYATL 780
Db 737 NHIFNSAIRKHLKSKTVLFTYHOLQYLVDCEYIFMKEGCITRGHEELMANGDYATL 796
QY 781 FNNLLGEPPEVINSKKESSGSKSODKPGTGSIKKEKAVKPEEGOLVOLEEGOGS 840
Db 797 FNNLLGEPPEVINSKKESSGSKSODKPGTGSIKKEKAVKPEEGOLVOLEEGOGS 856
QY 841 VPMSVYGVYIOAAGPLAFIYALFMLANGSTAFSTWMLSYWIKOGSNTVTYRGNETS 900
Db 857 VPMSVYGVYIOAAGPLAFIYALFMLANGSTAFSTWMLSYWIKOGSNTVTYRGNETS 916
QY 901 VSDSMKDNPMOYIASIVALSMAVMLLKAIRGVVEVKGTLRASSRLHDELFRILRSPM 960
Db 917 VSDSMKDNPMOYIASIVALSMAVMLLKAIRGVVEVKGTLRASSRLHDELFRILRSPM 976
QY 961 KPEFDTPTGRLNRFESKDNDEVNRLPFOAEMFIQNWIIIVFCVGMAGVFPWFIVAVGP 1020
Db 977 KPEFDTPTGRLNRFESKDNDEVNRLPFOAEMFIQNWIIIVFCVGMAGVFPWFIVAVGP 1036
QY 1021 LVTLFVLAHVSVRLIRELKRNDINOSPLSHITSSIOGLATIHANKOCEFLHROEL 1080
Db 1037 LVTLFVLAHVSVRLIRELKRNDINOSPLSHITSSIOGLATIHANKOCEFLHROEL 1096
QY 1081 LDDNOAPFLFTCAMRMLAVRDLISALITTTGLMIVLMHGOI PRAYAGLAISYAVOLT 1140
Db 1097 LDDNOAPFLFTCAMRMLAVRDLISALITTTGLMIVLMHGOI PRAYAGLAISYAVOLT 1156
QY 1141 GLFOFYRLASETEARFTSVERTNHITKTLSTLAPARIKKAPSPDMPDQGEVTFENAEK 1200
Db 1157 GLFOFYRLASETEARFTSVERTNHITKTLSTLAPARIKKAPSPDMPDQGEVTFENAEK 1216
QY 1201 RYREBNPLVLKVSFTIKPEKIGIVRTSGSSLSGMAJFRLVELSGGCIKIDGVNISD 1260

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Db 1217 RYREBNPLVLKVSFTIKPEKIGIVRTSGSSLSGMAJFRLVELSGGCIKIDGVNISD 1276
QY 1261 IGLADLRKSLSTIPQEPVLFSGTVRSNLDPFNOYTEDQIWDALERTHMECIIQOLPKLE 1320
Db 1277 IGLADLRKSLSTIPQEPVLFSGTVRSNLDPFNOYTEDQIWDALERTHMECIIQOLPKLE 1336
QY 1321 SEYMENDNFSVGEROLLCTARALLRHCKILLIDEAFAADTEFDLLIOETIEAFADCT 1380
Db 1337 SEYMENDNFSVGEROLLCTARALLRHCKILLIDEAFAADTEFDLLIOETIEAFADCT 1396
QY 1381 MLTIAHRLHTVLSDRIMVLAQGVVEFDPVSVLSSNDSSRFYAMFAAENKVAVKG 1437
Db 1397 MLTIAHRLHTVLSDRIMVLAQGVVEFDPVSVLSSNDSSRFYAMFAAENKVAVKG 1453

RESULT 3
US-08-843-459A-2
; Sequence 2, Application US/0843459A
; Patent No. 6162616
; GENERAL INFORMATION:
; APPLICANT: SHIJIAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHYTE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,459A
; FILING DATE: 16-Apr-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-056 (formerly MTL-001)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-4214
; TELEFAX: (617)227-7400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1453 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-843-459A-2

Query Match 99.9%; Score 7298; DB 4; Length 1453;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1277 IGLADLRSLKSLIIPOEVLVSGTIVNSNDPENOYEDQIMDALERTHMKECIAQLPLKLE 1336
QY 1321 SEVMENGDNFSGYEROLLCIARALLRHCKILLIDBATAAMDTEFDLLIOETIREAFADCT 1380
Db 1337 SEVMENGDNFSGYEROLLCIARALLRHCKILLIDBATAAMDTEFDLLIOETIREAFADCT 1396
QY 1381 MLTIAHRLHTVIGSDRIMVLAOGVVEEDTSPVLLSNDSRFYAMFAAENKVAVKG 1437
Db 1397 MLTIAHRLHTVIGSDRIMVLAOGVVEEDTSPVLLSNDSRFYAMFAAENKVAVKG 1453

RESULT 4
US-08-463-092B-4
Sequence 4, Application US/08463092B
Patent No. 5766880
GENERAL INFORMATION:
APPLICANT: Cole, Susan P. C.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MOLTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 435
FILING DATE: 8-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SRO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1531 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-092B-4

Query Match 28.5%; Score 2082; DB 1; Length 1531;
Best Local Similarity 34.5%; Pred. No. 2,5e-195;
Matches 488; Conservative 262; Mismatches 479; Indels 184; Gaps 21;

Query Match 28.5%; Score 2082; DB 2; Length 1531;
 Best Local Similarity 34.5%; Pred. No. 2.5e-195;
 Matches 488; Conservative 262; Mismatches 479; Indels 184; Gaps 21;

100 PYDNAGLFCSPMSLSTLARAHHKGGELMEDVNSLSKSHESDVCRCRLERMOELNE 159
 209 PSSASFLSRLTFWMTGLI-VRGYROPLEGSDLSLNKEDTSEOVVPLVKNMKKECK 267.
 160 V-----GPDAA-----SLRRVWIFCRTLIL 181
 268 TRKQPVKVVYSSKDDAQPRESSKYDANEVEALIVKSPQKEMNPSEFKLYTFPGYFLM 327
 162 STVCLMTIOLAGFSPAPFVKKLLLEYTOATESNLOYSLILVGLLITELVRSMSLALTA 241
 328 SFFFAIHDLMEFSGPO-ILKLLILEVNDTKAPDMOGYFYVLLPVTACLQVLVHQQYH 386
 242 INYRTGVLGAILTMAEKKILKNIKERS--LGLINICSDOORFMEAAGSLANG 299
 367 ICFVSGMRKTAVIGAVYRKALVITNSAKSSTVEIYVLMVDQREFDLATYINMWS 446
 300 GPVVAIIIGMITYVILGPTGLGSAVFILFYPMMFASHLTAFFRKCAVATDERVQKN 359
 447 APLOVILALYLMIMIGSVLAGVAVMVLVNAVMNAKTKTYQVAHMKSKDNRIKLMN 506
 360 EYLTIKFKIYAVYKAFSOSVOKIREERILKAGYFQSTIGVAPILVVIASVTPFS 419
 507 EILNIGIKYIKYAWELAKKDYALIROELKVKKSAVLSAGTFTWCTPFLVLCPTFA 566
 420 VHMILGFD--LTAOAFVTVVTFNSMTFALKVTPSVKSLSEASVAVDRFKSLFMEEVH 477
 567 YVITIDENNIILDAQTAFAFSLALFNILRPLNLPVVISIYQASVSKRLRIFLSHELE 626
 478 --MINKRASP---HIKEMKNATLAMOSSHSSIONSPLPKKKDKKASGKKEKYAQ 532
 627 POSIERRPVKGCGNSTIVRNATFTW----- 653
 533 LORTEHQAIVLEQKHLLDSDERSPEEBCKHILHGLRLQRTLHSDLEIOGKLVG 592
 654 -----ARSDP-----TLNGTTFESIPGALVA 675
 593 ICGSVSGKTSLSIALIOMQMLLEGSIAISGTFAYVAAOAMILNATLNDNIFGKEYDE 652
 676 VVGQVCGCKSSLSLALAMEKVEGHVAIKGSAVYPOAWIONSLRNLIFGQLEBP 735
 653 RYNSVNLGCCLRDLAIIIPSSDLTIGERGANSLSGQROKRSISLARALYSRSTIYLDPL 712
 736 YRSVIOACALLPDLLEILPSGDRTEIGEGVNLSSGQKORSILARAVYSNADIVLFDPL 795
 713 SALDAHVNHIFFNSAI--RKHLSKTVLFVPHOLOYLVDCCDEVIPMKGGCTIRGTHEEL 770
 796 SAVDAHVCKHIFENVIGKMLKNKTRILVTHSMYLPQOVDTIYVSGSKISEMSYDEL 855
 771 MNLNGDVATIF-----NNLL-----GETPVEIN 795
 856 LARDGAFAEPLRTYASTQEDAEENGVTYVSGPEKEAKOMENGLVLYDSAGKQOROLS 915
 796 SKRETSQOKSODKPTGSIKKKAVKPEBGQVLQLEKGGQSVPMVSVGYVIOAAG 855
 916 SSSSYSGDISRHHN---STAEIOKAEAKKETWKLMEADKQOTGVKLSYVDYKKAIGL 972
 856 PLAFILVALMLNVCASFSTMVLSWIKQSGNTYTRGNENSVSSMKDNPMQYTA 915
 973 FISELSIF-LPMCHVNSLANSYMLSTLTDPIYNGT---OEHRKVRSLVYGALISOGI 1028
 916 SIYALSMAMVLLKAIRGVVEVKGTLRASSRLHDELFRILRSPKFPDTPGTGILNRF 975
 1029 AVFGYNAVSI-----GGILASRCLHDLHLSILRSPMSFERPESGLVNRF 1076
 976 SKDNDEVAVRLPQAEFIOVNIIVFCVGMAGVFPWFLVAVGLVILFVSLHVSRL 1035
 1077 SKEDTVDMSIPEVILKMGMSLFNVIGACIYILLATPIAAILIPLGLIY---PFVQAFY 1133

1036 I---RELKRLDNTGSPPLSHITSSIQGLATTHAYKGGOEPLHROELDDNOAPEFLT 1092
 1134 VASSROLKRLIESRSRSPVSHFNETILLGVSVIRAFEEORFTHQSOLKADENOKAYPSI 1193
 1093 CAMRILAVRLDISALITTTGIMVIMHGOJPPAVAGALISAVOGLTLPQFTVLASE 1152
 1194 VANRMLAVLECVGNCIVLFAALFAVISRHSISAGLGVLSVSTLDVTTYLMVLMVMSSE 1253
 1153 TEARFTVERINHYIKTSLLEAPARIKNAKPSDPMQDEVEVFENAMRYRENPLVLAK 1212
 1254 METNIYAVERLKEYSET-EKAPWQJQETAPPSMWQVQVERBRNCLATREDLDVFLH 1312
 1213 VSFTRPKKIGTIGVGTSGKSSGLMALFRVYELSGGCIKIDGVRIISDGLADLSKLSI 1272
 1313 INVTTNGGKGVQIVGTGAGKSSLTGLFRINESAGEIIDIIGINIAKIGLHDLRKRITI 1372
 1273 IPOEPLFSGVSRNLDPNQOTEDQIMPALRTHMKECIADLPKLSEVENGDNFSV 1332
 1373 IPQDPLFSGSLRMNLDPSQTSDEEWTSLSLAHLDKVSALPDLDHECAGGGENLSV 1432
 1333 GEROLLICARALLRCKLILDEAPAMDETDLIOETIRBAFADCTMLTAHRLHTVL 1392
 1433 GOROLICARALLRCKLILDEAPAMDETDLIOETIRBAFADCTMLTAHRLHTVL 1492
 1393 GSDRIMVLAQGOVPERDTPSVLLSNDSSRFYAM 1425
 1493 DYTRVIVLDKGEIQEYGAPSDLL-QORGLFYSM 1524

RESULT 6
 US-08-460-907B-4
 ; Sequence 4, Application US/08460907B
 ; Patent No. 5891724
 ; GENERAL INFORMATION:
 ; APPLICANT: Dealey, Roger G.
 ; APPLICANT: Cole, Susan P.C.
 ; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
 ; TITLE OF INVENTION: RESISTANCE ON A CELL
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
 ; STREET: Queen's University at Kingston
 ; CITY: Kingston
 ; STATE: Ontario
 ; COUNTRY: CANADA
 ; ZIP: K7L 3N6
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/460,907B
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/029,340
 ; FILING DATE: 8-MAR-1993
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/141,893
 ; FILING DATE: 26-OCT-1993
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/407,207
 ; FILING DATE: 20-MAR-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: 08/141,893
 FILING DATE: 26-OCT-1993
 APPLICATION NUMBER: 08/407,207
 FILING DATE: 20-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: DECONTI, GIULIO A. JR.
 REGISTRATION NUMBER: 31,503
 REFERENCE/DOCKET NUMBER: POI-002CP8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1531 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-463-179A-4

Query Match 28.5%; Score 2082; DB 3; Length 1531;
 Best Local Similarity 34.5%; Pred. No. 2.5e-195;
 Matches 488; Conservative 262; Mismatches 479; Indels 184; Gaps 21;

QY 100 PVDNAGLESCMTFSLSLARVAHKKGELSMEDVMSLSKHESSDYNCRRLERLMOBELNE 159
 DB 209 PESSASFSLRTFWMITGLI-VRGYRQPLEGSDLSLNKEDTSEGVVPLVKNMKKECAK 267
 QY 160 V-----GPDAA-----SLRRVWVTECTRLLI 181
 DB 268 TRKQDPKVVYSKDPQAPQKRESSKYDANEVEALIVKSPQKEMNPISLFVLYKTFEPYFLM 327
 QY 182 SIYCMITQLAGSGPAPFVHLEETQATESNIQSLVYLGLLTTELVRMSLALPMA 241
 DB 328 SFFPKAIDIMAFSPQ-ILKLLIFVNDTKAPDMQGFYVTLLEVTACLOTLVHQQYFH 386
 QY 242 LNYRTGVRKALITLMAKRIILTKLNKES--LQELINICSDGQRFEEAAVSSLAG 299
 DB 387 ICFVSGMRITKAVIGAVYKALVITNSARKSSTYGEIYNLMSVDQRMDLATYINMIMS 446
 QY 300 GPVVAIIIGMIVNIIIGTGLGSAVFLTFYPAMMFASRLTAFFRKCAVATDERVQKMN 359
 DB 447 APILOYITLALYLLMLNLGVSVALGVAIVLVAVNAVMAMKTKTYOVAMKSKDNRIKILMN 506
 QY 360 EVLYTIFIKRYAWYKAFSOSVOKIREERERILEKAGFYOSTYTCVARIIVIVASVAFES 419
 DB 507 EILNGIVLKIYAMELAFKDVLAIRQBELKVLKKSATLSAVGTFTWCTPFLVALCTFA 566
 QY 420 VHMILGFD-LTAAQAFVTVTVFNSTFALKVTPFSYKSLSEASVAVDRFSLFMEEVH 477
 DB 567 VYVTIDENNIIIDAOFAFVSALFNLIRPLNILPMVYISSIVQASVSLKRLNIFLSHELE 626
 QY 478 --MIKNRPASP--HIKEMKATLANDSSHSIIONSFKLTPKMKKDKRASGKKEKYRQ 532
 DB 627 PDSTIERRPVVDGGGTNSTITVNAFTW----- 653
 QY 533 LQRTHEQAVLAEQKGHLLDSDERPSEEEGKHILHGLRLQRTLSIDLEIOEGKIYV 592
 DB 654 -----ASDDP-----TLNGITFSIEGALVA 675
 QY 593 ICGSVSGKTSLSAIIIGOMTLLEGSAISGTFAVVAQAAWILNATLNDLILFKEVDEE 652
 DB 676 VVGQVGGCKSSLSALLAEMDKYEGHVALKGSVAVVPOQAMIQDLSRENTLFCQLEEP 735
 QY 653 RYNSVLSNCCRLPDLALPSSDLTEIEBGCANLSGGQRORISTARALYSIDRSIYILDPL 712
 DB 736 YRSVSVIOACALPDLLEILPGSDRTIEIEKGVNLSGGQKOFVSLARAVYSNADITYLDDPL 795
 QY 713 SALDAHGNHIFNSAI--RKHLKSKYVLFTHOQYLVDCDEVTFMEGCTTEGTHBEL 770
 DB 796 SAYDAHGRKHIIFENVIPKGMKMKTKIILVTHSMYSYLPQVDYIIVMSGGKISEGYSQEL 855
 QY 771 MNINGDYATTF-----NNILL-----GETPPEVIN 795

DB 856 LARDGAFAEFLRTYASTEDQDAENGVTGVSQPGKEAKOMEGMLVTTSAGQOLORUS 915
 QY 796 SKKEISGQKKSODKPKGTGSIKKERAVRPEEGQIVLEEGKGGSVPMWYGVYIOAAG 855
 DB 916 SSSSYSGDISRHHN---STAELOKAEKKEETWKLEADKACQGVKLSVYMDYMAIGL 972
 QY 856 PLAFIVMALFMINVNSTAFSTWVLSYVNIKQSGNTTVRGNETSVSDMKDNPHQIYA 915
 DB 973 FIFSLIF-LFMCNHYVALASNLSWLSLWTDPLVNT---QETKYRLSVYALGISOI 1028
 QY 916 SIYALSMAYVLLIKAIRGVVVFVKGLRASSRLHDELFRRLSPMKFFPTPTGRILNRE 975
 DB 1029 AVGYISMAVSI-----GGLASRCLHVDLHLSILSPMSFFERTSGNLVNR 1076
 QY 976 SKDMDEVDRLPPOAMEFIONVILVEFCVGMAGVFPWFLVAVGPVLVILESVLHYRVL 1035
 DB 1077 SKELDTVDSDIMEPIVKMFMSGLFNFGACIVILLATPIAAIILIPGLIY---FFVQRY 1133
 QY 1036 I---RELKRLDNIOTSPFLSHITSSIQGLATHAYNKGGEFLHRYQELLDNQAPPELFT 1092
 DB 1134 VASSHQKRLSEVSNSPVYSHNETLLGVSIVIRAFEEQERFIHQSDLKVDENQAKYPSI 1193
 QY 1093 CAMRMLAVRLDLISIALITTTGTGLMIVLMGOLPAPVAGIATAYVOLTGLFOFTYRIASE 1152
 DB 1194 VANRMLAVRLDEVCYKCIYFALFAVISRHSLSAGLVGSLVSYSLQVTTYLLMVLPMSE 1253
 QY 1153 TEARTSVVERINHYIKTSLLEAPARIKNKAPSPDPOEGEVFEENAEKRENPFLVLK 1212
 DB 1254 METNIVAAVERLKEYSET-EKEAPMOIQETAPSSMPQVGRVFEFRNYCCRYREDLDFVLRH 1312
 QY 1213 VSFTIKPKKEKIGIVRTSGKSSLGMAFLRVLVLSGGCCIKIDGVNISIDGLADLSKSI 1272
 DB 1313 INVTLNGEKEKGVIGRTAGKSSLTGLFRINESAGEIILIDGINIARIGLIDLEFKITI 1372
 QY 1273 IPQEPVLFCGYRSMIDPFNOYTEDOIMDALERTHMKECIQPLKLESEVWENDNSY 1332
 DB 1373 IPQDVLFCGSLIRMLDPSQYSDDEVWTSLELAHLKQFVSLPKLKHCEGGENLSV 1432
 QY 1333 GEROLLICARALLRHCKIILIDEATAADTETDLIOETIRFAPADCTMLTIAHRLATVL 1392
 DB 1433 GORQLVCARALLRKTKILVIDEATAVADLETDDLIOGTIRQFDCIVLTIAHRLNITM 1492
 QY 1393 GSDRIMVLAQGVAFEDTPSVULSSDSSRYAM 1425
 DB 1493 DYTRVIVLDKGEIOXYGAPSDL-QQRLGFYSM 1524

RESULT 8
 US-08-461-384B-4
 Sequence 4, Application US/08461384B
 Patent No. 6025473
 GENERAL INFORMATION:
 APPLICANT: Cole, Susan P. C.
 APPLICANT: Deeley, Roger G.
 TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESS: Queen's University at Kingston
 CITY: Kingston
 STATE: Ontario
 COUNTRY: CANADA
 ZIP: K7L 3N6
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,384B
 FILING DATE: 05-JUN-95
 PRIOR APPLICATION DATA:

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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Mienicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01547
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1531 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-384B-4

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Query Match 28.5%; Score 2082; DB 3; Length 1531;
 Best Local Similarity 34.5%; Pred. No. 2,5e-195;
 Matches 488; Conservative 262; Mismatches 479; Indels 184; Gaps 21;

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QY 100 PVDNAGLCMTSWISLARVAHAKGELSMEDVYSLKSHSSDYNCRRERLMOEELNE 159
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 209 PESSASFLRITFWITGLI-VRGYRQPLSGSLMSINKEDTSQVAVPLVKNMKKCAK 267
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 160 V-----GDDA-----SLRRVWIFERTLIL 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 268 TRQOPKAVYSSKDPQPKSSKVDANEVVALIVKSPQKEMNSLKKVYKTFGPYFLM 327
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 SIYCLMTOLAGEGSPAFVWKHLEYQATSNLYSLVLGLLEIYRSMGLATWA 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 328 SPFFKAIHDLMMFSGPQ-ILKILIKFVNDKAPDMOGYFTVLLFYACLOTVLHOFH 386
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 LNRTRVRLGAILTYMAFKILIKLIKES--LGLINICSDNGQMFEEAAGSILAG 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 387 ICVSVGRITAVIYGAAYRRALVITNSARKSTVEIYNLSYDAQRFMDIATYINMWS 446
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 GPVAILIGMIVNIIIGPTGELSAVFIILFYPAAMFASRLATYRRRCVATDERVOKM 359
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 447 APLOVAILLTLMLNLSPSVLAGVAVVLMVPAVNAVMAKTKTYQVAMHMSKDRIRIKM 506
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 360 EVLTYIKFIMYAVKAFSOSVQKIREERRILEKAGYFQSIYGVAPIVVIASVTF 419
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 507 EILNGIKVLKLYAMELAFKRYALAIROBELKVLKKSAYLAVGFTWVCPIFLVALCTFA 566
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 420 VHMFLGFD--LTAQAFTVTVNSMTFALKVTPFSYKLSSEASVADRFKSLFIMEVH 477
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 567 VYVYTIENNLIIDAQFAVSLATFNILFPLNIIPLMVISIYQASVSFKRLRIFLSHELE 626
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 478 --MIKKNPASP--HIKIEKNATFLAWDSHSSIQNSPKILPKKKKRRKSRGKKEVQR 532
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 627 PDSIERPVDGGGTSITVRNAFTW----- 653
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 533 LQRTHOAVLAEGKHLILDSRSPSEEEKHILHGLRLQTLHSLIDEIOEGKIY 592
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 654 -----ARSDPP-----TLNGITFSIEGALVA 675
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 593 ICGSVSGKTSLSAILGOMTLLEGSLAIGTAPYVAQQAAMINATLRDNLFEKYEDEE 652
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 676 VVGQVGKSSLSALIAEDKVEGVAIKGSVAYVPOQAMIONDSIRENIIFCQCLEEP 735
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 653 RYNSVNSCCLRDIALTPSSDLTEIGERGANISGCGORISLARALYSRSTIILDDPL 712
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 736 YRNSVIOACALPDLPLTLPDREIGEKGVNLSGGQKORVSLARAVYSNADYILFLDDPL 795
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 713 SALDAVHGHIFNSAI--RRHLKSKVLFVTHQLOYLVDCDEVIFMKEGCTTERGTHEEL 770

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DB 796 SAVDAHVCKHIFENVIGKGLKKNKTRILVTHSMKSYLFOVDVYIIMSGKISKMSYDEL 855
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 771 MNLNGDYATIF-----NNLL-----GEPPEVEIN 795
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 856 LARDGAFAPFLRTYASTREQDAEENGVTYGVSGPQKAKQOMENGLVYDSAGKQLQROL 915
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 796 SKKETSQKRSQDKPRTGSIKKEKAVKPEEGQLVQLEEGGGSVPMSYGVYIQAAGG 855
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 916 SSSYSQGISRHHN--STAELQRAEAKKETWKLMEADKAQOTQVLSYWDYMKYALGL 972
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 856 PLAFVIALPLMLVNGSTAFSTWMLSYWIKGSGNTVTRGNETSVSDMNDPMQYXA 915
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 973 FISFLSLIF-LPMCHVSLAANYMLSLMTDPIYNGT--QEHKRVLSYVGAIGISGI 1028
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 916 SIYALSMVAWMLILKAIKRGVFEVKTLRASSRLHDELFRRLRSPPKEDTTPGRIINRF 975
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1029 AVFGYSMAVSI-----GILLASRCLHDLHSLRSPSPFERTPGCNLVNRF 1076
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 976 SKDDEVDVRLPQAEPIQAVIIFPCVSGIAGVFPFELVAVGPVILFESVHLVSKVL 1035
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1077 SKELDTVDSMTPEVVKMFMSGLFNVIGACIVILLATPIAATIIPLGLIY--FFVQRFY 1133
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1036 I---RELKRLDNTITOSPFLSHITSSIOGLATIHAYNKGQFLHRYOELLDDNOAPEFLT 1092
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1134 VASSROLKRLSEVSRSYSHFNETLGVSYIRAFEDERRIHOSDLKVDENOKAYPSI 1193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1093 CAMRWLAVRDLISALITTTGLMIVLHGOIPPAYAGLAISYAVOLTLGFQFTVRLASE 1152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1194 VANRWLAVRLECVCNCIYFALPAVVISRHSLSAGVLGSYSLSLOYTTVYNNLVYRMSSE 1253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1153 TEARFTSVYERINHIKLSLEAPARIKKNKASPPMPQGEVYTFEAKERYENRPLVYK 1212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1254 METNIVAVRLEKESER-EKAPWQIQTAPSSMPQVGRVREFRNYCIRYREDDEFLVLRH 1312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1213 VSFTIKREKIGIYRTGSGKSLGMAFLRVLVELSGGCIKIDYRISDIGLADLRSKLSI 1272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1313 INVYINGEKAGIYGRGAGSSLTGLFRINESAEGSIIIDGINAKITGLHDLRFKTI 1372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1273 IPQEPVLESGTVRSNLDPEFNOYTEDQIWDALERTHMKRCIAQLPKLISEVMEGDNFSV 1332
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1373 IPQEPVLESGTVRSNLDPEFNOYTEDQIWDALERTHMKRCIAQLPKLISEVMEGDNFSV 1432
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1333 GEROLCIARALLRHCKLILIDEAPAMDPTDILLQITTEAPADCMILTAIRHLVYL 1392
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1433 GQROLVCLARALKKTKILVDEATAVADDETDLIDISTIFQEDCTVITIAHRLTIM 1492
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1393 GSDRIWLAQGOVVEFDPSPVLSNDSRFFYAM 1425
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1493 DYTREVYLDKGEIDYEGAPSDL-QQKGLPFSM 1524
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 9
 US-08-141-893-2
 Sequence 2, Application US/08141893
 Patent No. 548519
 GENERAL INFORMATION:
 APPLICANT: Deeley, Susan P.C.
 APPLICANT: Deeley, Roger G.
 TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 STATE STREET, SUITE 510
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25

Query Match	28.4%	Score 2075	DB 1	Length 1531
Best Local Similarity	34.5%	Pred. No. 1.2e194		
Matches 487	Conservative 261	Mismatches 481	Indels 184	Gaps 21

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0Y 100 PVDNAGTSCSMFWSLMSIARVAHKKGELSMEDWMSLSKSHSSDVCNCRLELMQOEELNE 159
Db 209 PESSASFSLRITFWMITGLI-VRGTRPQLESGDLSLNKEDTSEQVVPVLYVMNKKCAK 267
QY 160 V-----GPDAA-----SLRRVWVJFCRTRLI 181
Db 268 TRKQPVKVVYSSKDBAPEKSESSKVADNEVEALIYKSPQKEMNPISLFKLYTFCGPFLM 327
QY 182 SLVCLMTIOLAGFSPPAPVWKHLLTYQTATESNLQYSLILVGLLTELIVRSWSIALIYWA 241
Db 328 SFEFAHIDHLMFSSGPQ-ILKLILIFVNDTKRPMQGFYVILVELVTCLOTLVLVHQVFN 386
QY 242 INYTRGVRLGALITMAFKRIILKTIKRIKES--LGEILINCSNDORMEEAAYSLAG 299
Db 387 ICFVSGMKIKRIVAGIYVRKALVITNSARKSSTVEIYMLKSVDMQOREPDLATYINMTWS 446
QY 300 GPVVAIILOMIYVITLIGPTGLSGAVFTLEFPAMMFASHLTAYFRKKCYAATDERVOXKN 359
Db 447 APLOGLIALLYLMLLIGSVLAVGAVVMLVAVMLVAVNVAAMKRTQYVAHMKSDNRKILMN 506
QY 360 EYLYTRIKIKYAWKAKSOSQYKTRREERRLLEAGFQSTTVGVARPLYVVIASVYFS 419
Db 507 ELINCIKYLKIYAMLEAKRDKVALROBELKKLKKSATLSAAGTPTWCTPPLVALCTFA 566
QY 420 VHMTLGDF--LTAAGAFVTVTFVFNEMTALKTPEFSKSLSEASVAVDFKSLFAMEEH 477
Db 567 YVVTIDENNIIIDQAFAFVSLAFNLRRPINLIPVSIISYQASVSLKRLRIFLSHELE 626
QY 478 --MIKNKASP---HIKTEMKNATLAWDSHSSSIONSPKLTPMKKDKRASHGKKEVQO 532
Db 627 PDSIERRRPVKDGGSNTSITVRNATFTW----- 653
QY 533 LQRFHQAIVLAEQKHLLDDERSRPEEBEKHHLGLRLQRLHSDLEIQGKLVG 592
Db 654 -----ARSDPP-----TLNGITFSPGALVYA 675
QY 593 ICGVSGSKTSLISAILGOMTLLSESIASIGTFAVVAQOAMITLNTDNLIFKEYDEB 652
Db 676 VVGQVGCGCKSLISALLAEMKVEBHAIVKISVAIVPQOATQONDSKRENILFGQLEBP 735
QY 653 RYNSVYNSCCRLPDLAIPSSDLEIGERGANLSGGQRQISLALARYSDRSIYLLDDPL 712
Db 736 YRYSYIQCACALLPDLIELIPSGDREIEGEGVNLSGGQRQVSLARAAYVSNADITYLDDPL 795
QY 713 SALDAVGNHNFNSAL--RKHLSKSTVLFYVHOLQYLVDCDEYIFMKGSGCITERGTHEEL 770

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[illegible]


```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1531 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-092B-2

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Query Match      28.4%; Score 2075; DB 1; Length 1531;
Best Local Similarity 34.5%; Pred. No. 1,2e-194;
Matches 487; Conservative 261; Mismatches 481; Indels 184; Gaps 21;

QY 100 PVDNAGLFCMTFSWTLSSARVAHKKGELSMEDVWSLSKSHSSDVNCRRLERLMOEELNE 159
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 209 PESSASFSLRITFWITGLI-VRGYRQPLEGSDLSLNKEDTSEQVAVLVKMKKCEAK 267
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 160 V-----GPDAA-----SLRRVWICRTLLIL 181
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 268 TRKQPVKVVYSSKDPQPKRESSVVDANEVEVALIVSPQKEMWSPLEKVLKTFPGPYFLM 327
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 182 SIYCLMITOLAGSGPAFMVKHLELYTOATESNLOYSSLVLGLLLEIYRSMGLATWMA 241
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 328 SEFFKAIHDLMTSGFO-IKLIKIPVNDTKADPMQGYFTYVLLFTYACLOTLVLHQYEH 386
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 242 LNTRGVRLGAILTYMAFKKILKLIKIKES--LGELINICSDGQRMFEAAVGSLLAG 299
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 387 ICSVSGMRITAVIGAVYRKALVITNSARKSSVGEIIVNLMSYDAQGFMDLATYINIMWS 446
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 300 GPVVALLIGMIYNYIIIGPTFLGSNAFIFYPPAMFASRLTATFRKCVAAATDERVOKM 359
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 447 APLOVILALVLLMLNLPGLPSYLAGVAAVLVVYNAVAMKTKYOVVHMSKDNRIKILMN 506
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 360 EVLTYYIKFIKMYAVKAFSOSVOKIREEERRIIEKAGYFOSITVGVAFIVVAVTASVTF 419
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 507 EILNGIKVLKLYMELAFKRYALAIROEELKVLKKSAYLSAVGFTWVCPTFLVALCTFA 566
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 420 VMTLIGFD--LTAAGFTVTVTVNSMTFALKVTPFSVKSLSSEASVADREKSLFMEVH 477
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 567 VYVYIDENNILDAQTAFVSLATFNILFPLNIIIPMVISSIVQASVSLKRLRIEFLSHELE 626
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 478 --MIKKPASP---HIKIEKNATLAMDSSHSSTIONSFKLLPKMKKKRRASRGKKEVRQ 532
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 627 PDSIERPVPVDDGGTNSITFRNATFTW-----653
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 533 LQSTHOAVLAEQKGLHLLDSDRPSPREEEGKHILGHILRLQRTLHSLDLEIQEGKLVG 592
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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DB 654 -----ARSDPP-----TLNGITFISIEGALVA 675
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 593 ICGSVSGKTSLSAIIIGMTLLEGSLAIGSTFAFYVAQAMILNATLRDNLTPCKEYDEE 652
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 676 VVGVGCGGKJLSLALLAEWDKVEGHAIRGSVAVYVQQAQNDLSRENTLFCQLEEP 735
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 653 RYNSVLSCCRLPDLALIPSSDLEIGERGANLSGQORORISLARALYSPRSIYILDDPL 712
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 736 YRVSVIQACALLPDLLELIPSDRREIEGKCVNLSGQKORSLARAYSNADYILFPDPL 795
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 713 SALDAVGNHIFNSAI--RRHLKSTVLEVTYHOLQYVDCDEVIFMKEGCTTERGTHEL 770
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 796 SAYDAVGHKHFENVIGPKMKLKNKTRILVTHSMYSYLPQVDVILYMGSGKISEMGYQEL 855
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 771 MNLNGDYATIF-----NLLI-----GEPPEPEIN 795
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 856 LARGAFAEPLRYASTEQEDAEENGVTYVSGPKREAKOMENGMVYDSAGKOLQRLS 915
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 796 SKKETSQKKSODKGGKRTGSIKKREKAVRPEQOLVLEEGKGSVPMSVGYVIOAAG 855
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 916 SSSYSGDISRHN---STAELOKAEAKREBTWKLEADKQOTQOVKLSYWDKMAIGL 972
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 856 PLAEVIMALEMLNVGSTAFSTWMLSYWIKOGSGNTTVTRGNETSVDSDMKNDPMOYVA 915
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 973 FIFLSIF-LFMCNHSALASNYWLSMTDDPIYNGT---QETHKRVLSYVGAIGISQGI 1028
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 916 STYLSAAMVILKAIKGVYFVKGTLRASSLHDELFRILRSKMFEDTTPGRIILNR 975
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1029 AVEGYSMAVSI-----GGILASRLHDLHLSIRSPSEFEFRPSGNLVNRF 1076
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 976 SKMDEVDAVRLPQAEFIONVILVFCVGMIAGVPMFLVAVPVLVILFSLIVSRVL 1035
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1077 SKELDTYDSMTPEYIKKFMGSLFNVIACIYILLATPIAIIIPPLGITY---FFVQRFY 1133
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 1036 I---RELKRLDNTQSPFLSHITSSIOGLATIAHYNKQGEFLHRYOELLDDNQAPFLETT 1092
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1134 VASRQKRLRESVSRPSYSHFNETLLGVSYIRAFEEQERIRHQSOLKVDENQKAYPSI 1193
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 1093 CAMWLAVRDLISALITTTGLMIYVLMHQIIPRAYGLAISYAVOLTGLFQFYVRLASE 1152
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1194 VANFMIAVRLECGVNCCLVLAFLPAFVISRHSLSAGLVGLSVSYSLQVYTTVMVLRMSSE 1253
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 1153 TEARFTVERINRYIKTSLSEAPARKKAPSPMPQEGEYTFNAEKRYENPLPLYVK 1212
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1254 METNIYAVERIKESSEI-EKAPMOIOTETRPSSMPQVGRYEFNNYICLRATEDLPYLKH 1312
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 1213 VSEPIKREKIGIVRTSGKSSIGMALFRLVELSGGCIKIDYRISDIDIGLADLRKLSI 1272
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1313 INVYINGEKGVIGRTGAGKSSLLTGLFRINESAGEIILIDGINIAKIGLHDLRFKITI 1372
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 1273 IPOEVLPESGVTSNLDPPNOYTEDQIWDALERTHMECIAQLPLKLESEVMENGDNFSV 1332
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1373 IPODPVLFSGSLRNNLDPPFSQYSDSEYVTSDELHLKDPVSALDPDKLDHCEAEGEENISV 1432
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 1333 GEROLLCAIARLLRHGCLLILDEATAMPDETDLLIOETREAPADCTMLTIARLHTVL 1392
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1433 GQROLVCLARLLKRTKTLIVLDEATAVVDETDLDISTIFQEDCTVLIARLNTIM 1492
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 1393 GSDRIWLAQGOVVEFDPVSILLNDSRSRYAM 1425
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1493 DTYRVIYLDKGEIDYCAPSDL-QQRLGPFYSM 1524
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 11
US-08-462-109A-2
; Sequence 2, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; MULTIDRUG RESISTANT TUMOR CELLS

```

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NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,109A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/441,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: P01-002CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1531 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-109A-2

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Query Match 28.48; Score 2075; DB 2; Length 1531;
Best Local Similarity 34.58; Pred. No. 1.2e-194;
Matches 487; Conservative 261; Mismatches 481; Indels 184; Gaps 21;

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QY 100 PVDNAGLFCMTFESWLSLAVAHKKGELSMEDVWSLSKSHSSDYNCRRLELMQEEINE 159
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QY 160 Y-----GPDAA-----SLRVVWIFCRLIL 181
DB 268 TRKQPVKVVYSSKDPAPQPKESKSKVDANDEVALIVKSPQKEMNPSLEFVLKKTGPPFLM 327
QY 182 STVCLMTTQLAGSGPAPFVWKHLELYQATESNLQYSLILVILGLTEIVWSMIALTWA 241
DB 328 SFEFKAIHIDLMFSGPQ-IKLKIKFVNDFKAPDMQGFYVLLFVACLOTIVLHQYFH 386
QY 242 LNTYTGVRIGAILTMAFKTLIKLNKES--LGEILNICSNDGQRFEEAAVAGSLAG 299
DB 387 ICFVSGMRITTAIVGAVYRALVITNSARKSSIVGEIINILMSVDAQFEMDLATYINMWS 446
QY 300 GPVAAILGIMYINVIILGTGFLGSAVFLIFPAPMMFASRLTAHYRRKCVATDERVOKN 359
DB 447 APLOVIALILVIMLNLGPSTVLAGVAVVLAIVPAVAMMKTKTYOVAMHMSKDRIRKLN 506
QY 360 EVLTLYIKFIMYAVKAFSOSVOKIREERRIIEKAGYFOSITVGVAPIVVIVIASVTF 419
DB 507 EIIINGIKVLKIAMELAFKQVLAIRQELKVLKKSAYLSAVGFTWVCIPPELVATFEA 566
QY 420 VHTLIGFD--LTAQAFTVTVFNSMTFALKVTPESVKSISEASVAVDRKSLFLEMEVH 477
DB 567 VYVTIDENNITDAQTAFAVSLATFLNIFPLNITLPMVIVISSIVQASVSLKRLRIFLSHELE 626

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DB 654 -----AKSDP-----TLNGTFFSIPEGALVA 675
QY 593 ICGSVSGKTSLSLAILGQMTLEGSIAISGTFAYVAQOAMILATLRNILEGKEYDEE 652
DB 676 YVGQVCGKLSLISALLAMDKVEGHVALKGSVAYVPOQAMQNDSLRNILLFGCQLEEP 735
QY 653 RYNSVNSCCLPDLAILPSSDLTEIGEGANISGGQROPISLARALYSDRSLYILDDPL 712
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DB 796 SAVDAHVGHIFENYVIGPKMLNKTRILVTHSMSTLPQVDVILVWSGGKISEMSYQEL 855
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DB 916 SSSSYSGDISRHHN---STAELOKAKEAKEETWIKMEADKQGTQGVKLSVYDMYKAIGL 972
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DB 1433 GOROLVCIARALLRKRTILVDEATAVADLETDDLIOSTIRQEDCTVLTIARIMTIM 1492
QY 1393 GSDRIMVLAOGVVEFDTPSVLLSNDSSRFAM 1425
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RESULT 12
US-08-460-907B-2
; Sequence 2, Application US/08460907B

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? Patent No. 5891724
? GENERAL INFORMATION:
? APPLICANT: Deeley, Roger G.
? APPLICANT: Cole, Susan P.C.
? TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: PARTHO RESEARCH & DEVELOPMENT INNOVATIONS
? STREET: Queen's University at Kingston
? CITY: Kingston
? STATE: Ontario
? COUNTRY: CANADA
? ZIP: K7L 3N6
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: ASCII text
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/460,907B
? FILING DATE: 05-JUN-1995
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/966,923
? FILING DATE: 27-OCT-1992
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/029,340
? FILING DATE: 8-MAR-1993
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/141,893
? FILING DATE: 26-OCT-1993
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/407,207
? FILING DATE: 20-MAR-1995
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Steeg, Carol Miernicki
? REGISTRATION NUMBER: 39,539
? REFERENCE/DOCKET NUMBER: Q1551
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (613) 545-2342
? TELEFAX: (613) 545-6853
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1531 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-460-907B-2

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Query Match      28.4%; Score 2075; DB 2; Length 1531;
Best Local Similarity 34.5%; Pired. No. 1,2e-194;
Matches 487; Conservative 261; Mismatches 481; Indels 184; Gaps 21;

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QY 100 PVNAGLFCMTFSWLSLARVAHKKGELSMEDVWSLSKHESSDVNCRLERLMQEELNE 159
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QY 160 V-----GPDAA-----SLRVVWIFCRRLIL 181
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DB 268 TRKQPVKVVVSSKDPAPKRESSVDANEVEALIVKSPQKEMNSLFKVFYKFGPYFLM 327
QY 182 SYICIMTTOAGSGPAFWFKHLLVYQATSNLQYSLLLVIGLLLEIRVMSALTLMA 241
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DB 328 SFFPKAIHDLMSGSPQ-IILKLIKRYNDTKAPDMQGYFTYVLLFVACIQTLVLAQYFH 386
QY 242 LNRGTGRLGAILTYMAFKILKLIKTKERS--LGELINICNDGQMFEEAAVAGSLLAG 299
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QY 360 EVLTYYIKIKMYAVAKFASQSVQKIREERIRILEKAGYPOSITVGVAPIVVIVASVTF 419
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DB 507 EILNGITVILKLYAMELAFKPKVLAIRDBELKVKKSIVLASVNGFTVWCPIFLVALCTFA 566
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DB 567 VYVYIDENNIIIDQTAFAVLSALFNILRFLNIIIPMVISSIYQASVSLKRLRIFLSHELE 626
QY 478 --MIKNRPASP--HIEIKNKATLADSSHSIIONSPKILPKKKKKRKRKKEVYRQ 532
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QY 533 LQRTHQAVLAEQGHLLDSDERSPEEREGKHILGHILRLQRTLSIDLEIOEGKLVG 592
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QY 653 RYNSVLNSCCRPDLALPPSSDLTEIGERGANLSGGORISLARALYSDRSIYIILDDL 712
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QY 713 SALDAVGNHIFNSAI--RKHLKSTVLFYTHOQYVDEDEVFMKEGGTTERGTHEEL 770
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QY 771 MNINGDYATTF-----NNILL-----GETRPVEIN 795
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QY 856 PLAFVYMALFPLVNGSTAFSTWMLSYWIKOGSGNTVTGNGENSVSDSKNDNPHQYUA 915
DB 973 FISFLSTF-LPMCNHVSALASNTWLSLMTDDPYNGT--QEHTKVLSYVAGLIGISOGI 1028
QY 916 SIYALSAVAMLILKAIRGVVFKGTRASSRLHDELFRILRSPMKFEFTPTGRILNRF 975
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QY 1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGOIPAVAGLAISYVAVOLTGLFQFVTRALASE 1152
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DB 1194 VANRWLAVRLDCEVNGCIVLFAALFAVISRHSLSAGLVGSYSLOYTTTLNMLVYRMSSE 1253
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 Db 1493 DTRVIVLKDGEIOEYGAPSDDL-QORGLFYSM 1524
 RESULT 13
 US-08-463-179A-2
 Sequence 2, Application US/08463179A
 Patent No. 6001563
 GENERAL INFORMATION:
 APPLICANT: Cole, Susan P.C.
 APPLICANT: Dealey, Roger G.
 TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,179A
 FILING DATE:
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/966,923
 FILING DATE: 27-OCT-1992
 APPLICATION NUMBER: 08/029,340
 FILING DATE: 8-MAR-1993
 APPLICATION NUMBER: 08/141,893
 FILING DATE: 26-OCT-1993
 APPLICATION NUMBER: 08/407,207
 FILING DATE: 20-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: DeConti, Giulio A. Jr.
 REGISTRATION NUMBER: 31,503
 REFERENCE/DOCKET NUMBER: POI-002CP8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1531 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-463-179A-2
 Query Match 28.4%; Score 2075; DB 3; Length 1531;
 Best Local Similarity 34.5%; Pred. No. 12e-194;
 Matches 487; Conservative 261; Mismatches 481; Indels 184; Gaps 21;

Db 328 SEFFRAIHDLMAFSGFO-LTKLTKFVNDTKAPDMOGIYYVLLVNTACLOTLVHOFH 386
 QY 242 LNYRTGVRLLGAILTMAFKKILKLNKIKES--LGLNLINCSNDQRMFEAAVSLLAG 299
 Db 387 ICFVSGMRKTAIVAGAVYKALVITNSARKSSVGEIVNLMSVDQRFMDLATYINMWS 446
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 QY 1393 GSDRMVLAOGVVEEDFPSSVLLSNDSSRPYAM 1425
 Db 1493 DYTRVIVLDKGEIYQEGAPSDLL-QQRGLFYSM 1524
 RESULT 14
 US-08-461-384B-2
 Sequence 2, Application US/08461384B
 Patent No. 6025473
 GENERAL INFORMATION:
 APPLICANT: Cole, Susan P.C.
 APPLICANT: Deleley, Roger G.
 TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
 STREET: Queen's University at Kingston
 CITY: Kingston
 STATE: Ontario
 COUNTRY: CANADA
 ZIP: K7L 3N6
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 FILING DATE: 20-MAR-1995
 ATTORNEY/AGENT INFORMATION:
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 REGISTRATION NUMBER: 39,539
 REFERENCE/DOCKET NUMBER: Q1547
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 TELEPHONE: (613) 545-2342
 TELEFAX: (613) 545-6853
 INFORMATION FOR SEQ. ID NO. 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1531 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-461-384B-2
 Query Match 28.4%; Score 2075; DB 3; Length 1531;
 Best Local Similarity 34.5%; Pred. No. 1,2e-194;
 Matches 487; Conservative 261; Mismatches 481; Indels 184; Gaps 21;
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 Db 209 PESSASFSLRITFWITGLI-VRGYROPLEGSGLMSLNKEDTSEGVVPLVYKMKKKCAK 267
 QY 160 V-----GPDAA-----SLRRVVICRTRLIL 181

Db 268 TRKQPVKVVYSKNDPAQPKRESKVDANEVEALIVKSPQKEMNPSEKVLVYKTEGPFYELM 327
 QY 182 SIYCLMTIOLAGSSGPAFMVKHLETOATESNLOYSLLVGLLLEIYRSNSLALTWA 241
 Db 328 SFFPKAHLHDMFSGPO-ILKLILKEFVNDKADPMOCGYFYTVLLFVYACQITLVLMHOYFH 386
 QY 242 LNRITGVRLGAILTLMFAKILKLNKIKES--LGELINCSNDGOMFEAAVGSLLAG 299
 Db 387 ICEVSGMRKTAIVAGYARRALVITNSARKSVYGEIVNLMSYDAQFMDLATIYINNIWS 446
 QY 300 GPVVAIIGMIYNYIILGPTGELSAVFIIFYPAMFEASRLTAFFRRKCVATDERVOKM 359
 Db 447 APLOVILAILLMLNLGSPVLAVAVVAVLVPAVNAVMAKTKTYQVAHMSKDNRIKLM 506
 QY 360 EVLTLYIKFMVAVKAFSOSVOKIREERRILEKAGYFOSITVGAIVVIVIASVYTES 419
 Db 507 EILNGIKVLKYLAMELAFKDKVLAIRQEEILKLSAYLSAVGTFTVWCPTPLVALCTFA 566
 QY 420 VHMILGFD--LTPAQAFVTVVNSMTFALKVTPFSYKSLSEASVANDRKSLFMEVH 477
 Db 567 VVYVITDENNLIDQATAVSLATFNILFPNLIIPMVISIVQASVSLKRLRITLSHELE 626
 QY 478 --MIKNKPASP--HIKEKKNATLWMDSSHSIIONSPLTPMKKKDKRASRCKEKVRQ 532
 Db 627 PDSIERRPVVDGGGTSITVYRNATFTY----- 653
 QY 533 LQRTHOAVLAEOKHLLDSDERSPEEBEGRHILGLRLORTLSHIDLEIOEGKLVG 592
 Db 654 -----ARSDPP-----TLNGITFISPEGALVA 675
 QY 593 ICGSVSGKTSLSAILIGOMTLLGSAISGTRAYVAQAMINLATRDNILGKEVDEE 652
 Db 676 VQVQVGGKLSLSALAEKDKVGHAIKGVAYVQQAIDQSDSRENIIFGQOLEEP 735
 QY 653 RYNSVLNSCCRLPDLALIPSDLTEIGERANISGGORQRTSLARALYSRSIYILDDPL 712
 Db 736 YKRSVIOACALLDLDELTPSGDRTGEIGKENVLSGGQKQVSLARAYSNADITLFPDPL 795
 QY 713 SALDAVGHNIENSAT--RKHLSKTVLFTVHOLQYVDCDEVIFMKESCITERGTHEEL 770
 Db 796 SAVDAVGHKIFENNVIGPKMLKTKRILVTHSMSTLPQVDVILVMSGKISEKSYOEL 855
 QY 771 MNLNGVYATIF-----NNLL-----GEPPEIN 795
 Db 856 LARDGAFAEFLRTYASTQBDQDAEENGVTGSGPKAKOMEGMLVTDGAGQLOLQRLS 915
 QY 796 SKKETSGSKSODKGPKTGSIKKKAVKPEECOLVLEKGGGSPWVYGVYIOAAG 855
 Db 916 SSSYSQSDISRHN---STAELOKAKEKKEETWKLMADKAQIQGVKLSYVMDYKRAIGL 972
 QY 856 PLAFVYLMALFNLVNSTAFSTWMLSYWIKQSGNTVTTRGNETSVSDSKNDPHMOYVA 915
 Db 973 FISFLSIF-LFMCNHNVALSNWYLSLMTDDPIYNGT--QEHTRKVLVSYGALGISOGI 1028
 QY 916 SIYALSMVAILLKATRGVVFVGTLRASSRLHDELFRLLRSPMKRFDTPPGRIINRF 975
 Db 1029 AVFGYSMAVSI-----GGILASRCLHVDLHSLIRSPMSFEPTSGNVLNRF 1076
 QY 976 SKMDDEVYRLPFOAEFIONVILVFCVGMIGVFPMPFLVAVGPIVLSVLHIVSRVL 1035
 Db 1077 SKELDLYDSMIFEVYIKKFMGSLRNIVIGACIVILLATITIAIITIPPLGLIF---FFVQRFY 1133
 QY 1036 I---RELKRLDNTIQSPLSHITSSIOGLATTHAYNKGOEFLHRYOELLDNDQAPFFLFT 1092
 Db 1134 VASSRQKRLIESVRSRPSYTHFNFTLIGVSVIRAFEEQREFIRHSDLKVDENQKAVPSI 1193
 QY 1093 CARRMLAVRLDISALITTTGLMIVLMHGOIPRAYGLAISAVOULTGLQFTVRLASE 1152
 Db 1194 VANRWLAVRLECVGNCTVLPALPAVTSRHSLSAGVLSVSYLOVTTTLLNMLVWRMSE 1253
 QY 1153 TEARFTSVERINHYIKTSLSEAPARIKNKAPSPDMPOEGVTFEENAMRYRENPLVLK 1212

Db 1254 METNIVAEERLEKEYSET-EKEAPMOIOETRPSPSPVPOVGRVFEFNNVCLTRREDDPVLH 1312
QY 1213 VETIKPREKIGIVGTSGKSSLSGMALFELVLESGGCKIDGVASISDGLADLSKSI 1272
Db 1313 INVTNGEKYIVGTGTAGSSSLTGLFRINESAGEELIIDGINIAIKGLHDLFKITI 1372
QY 1273 IEOEVLEFSGVRSRLDPNOYTEDOIMDALERTHMEKICIAIPLKLESEVENGDNSV 1332
Db 1373 IEDPVLFGSGLRMLDPFSQYSDEEVTSLMLHKLQFVSLDPKLDHECAGEGENLSV 1432
QY 1333 GEROLLICARALLRHCKLIIIDEATAADTETDLIIQETIEAFADCTMLTAHRLTVL 1392
Db 1433 GOROLVCLARLLKRLKTLVLEATAAVALDETDLIOSTIETFOEDCVLTIAHRLTIM 1492
QY 1393 GSDRIMVLAQOVVEFTPSVLSLSDNSRFYAM 1425
Db 1493 DYFVIVLDKGEIGEGAPSDL-QORGPIISM 1524

RESULT 15
US-08-407-207A-2
Sequence 2: Application US/08407207A
Patent No. 46063621
GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,207A
FILING DATE: 20-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Mternicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01512
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1531 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-407-207A-2

Query Match 28.4%; Score 2075; DB 3; Length 1531;
Best Local Similarity 34.5%; Pred. No. 12e-194;
Matches 1487; Conservative 261; Mismatches 481; Indels 184; Gaps 21;

QY 100 PVNAGLFCMTFSWLSLARVAHKKGELMEDVWLSLSKHESSDVNCRRLERLQOEELNE 159

Db 209 PESSASFSLRITFMWITGLI-VRGYRQPLEGSDLSMLNKEDTSBOVVPVLVKNMKKECAK 267
QY 160 V-----GPDAA-----SLRWVMECTRLIL 181
Db 268 TRKQPVKVVYSSKDDPAQKRESKVDANEVEALYKSPQKEMNPSLFVLYKTFGPFLM 327
QY 182 STVCLMTQLAGFSGPAPMVKHLLEYTOATESNLQYSLVLGLLTTELIVSWSLALTW 241
Db 328 SEFFKAHIDLMFSGPO-ILKLLIKFVNDTAPDMQGFYVLLFVTAICLOTLVHOFYH 386
QY 242 LNYRTGVRLRALILTMARKILKLNKEKS--LGELINISNGDGRFEEAAVAGSLAG 299
Db 387 ICFVSGMRKITYAVGAVRKALVITNSARKSSGVEIYNLSVDAQRFMDLATIINMWS 446
QY 300 GPVVAILGMIYVNIILGPTGLGSAVLEFFTPAMMFASRLTAIRKCAVATDERVQKN 359
Db 447 APLOVITLALVLLMLNLGSPVLAGVAVNVLAVNANVAMKRTQYVAHMKSKDRIRIKM 506
QY 360 EVLTYIKFKYAWVAKFQSOSVQKIREBERILEKAGYFOSITVGVAPIVVIVASVTF 419
Db 507 EILNGIKVLYKLAWEALFKDKVLAIRQELKVLKKSATLSAVGFTWCTPFLALCTFA 566
QY 420 VHMILGFD--LTAQATVTVTVNSMTFALKVTPFSVKSLEASAVADRKSFLMEVH 477
Db 567 VYVITDENNLIDQTAFAVSLALFNILFPLNIIPLMVISIYQASVSLKRLIRIFLSHELE 626
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QY 533 LQRTHOAVLAEOKGHLLDSDRSPSEERKHIHLRLORTLSIDLEOBEKING 592
Db 654 -----ARSDP-----TLNGITFSPICALVA 675
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Db 676 VVGQVCGKRLSLSLALAEKDKVEGHVAIKGSVAVYPOQAMIONDSLRNILEFCOLEEP 735
QY 653 RYNSVNSCCLRPDALILPSSDLTEIGERGANAISGQORISLARALYSDRSYIIDPL 712
Db 736 YRSVIAQACALLPDLIELPBGDTETGERGVNLSGGOKORVSLARAVYSNADYILEDDPL 795
QY 713 SALDAHVGNHIFNSAI--RKHLSKTVLFVTFQLOLVYDCDEVIFPKBECCITERGHEEL 770
Db 796 SAVDAHVGKHFENYIGPGLMKNTRLIYTHSMSTLPDQVYIYVSGGKISEMSYQDL 855
QY 771 MNLNDYATIF-----NNLL-----GETPPEIN 795
Db 856 IARDGAFEFELRTYASTEOEDAEENGVTGVSQPKKAKOMENGMVLYDSAKOLOROLS 915
QY 796 SKKETSGSOKSODKGPRTGSIKKKKAYKPEGOLVLEEKGGSVPSVGVYIOAAGG 855
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QY 916 SIYALSAVMILAKIRGVVYVKGTLRASSRLHDELFRILIRSPKPFDTPTGRIILRF 975
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QY 1036 I---RELKRLDNTIQSPFLSHITSSIOGLATIHAYNKGOFELHRYOELDONQAFLELT 1092
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QY 1093 CAMRWLAVRLDISALITTTGMLVLMHGOIPPAYAGLAISYAVOLTGLFOFTVLRLASE 1152
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QY 1213 VSEPTIKPERKIGIVRTSGSGSSIGMALFRLVELSGGCIKIDGVRIISDIGIADLRKLSI 1272
Db 1313 INVTINGGEKVGIVGRTGAGKSSLTGLFRINSAGEEIIIDGINIAKIGLHDLRFKITT 1372
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Db 1373 IPODPVLFSGSLRMNLDPFSSQYSDDEEYMTSLIELAHLKDFVSALPDKLDHECAEGENLSV 1432
QY 1333 GEROLCICARALRHCKIILIDEATAAMDRETDLLIOETIREAFADCTMLTIAHRLTVL 1392
Db 1433 GORQLVCLARALKTKIKILVLDATAVADLETDLLIOSTIRTOFEDCTVLTIAHRLNTIM 1492
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Search completed: August 11, 2002, 11:08:49
 Job time: 6524 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2002, 09:20:50 ; Search time 183.28 Seconds
(without alignments)
2759.690 Million cell updates/sec

Title: US-09-528-031-2

Perfect score: 7308
Sequence: 1 MKDDICKEITIPSGYRSV.....DSSRFYAMFAAEKAVKVG 1437

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending-Patents-AA-Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	7308	100.0	1437	19	US-09-528-031-2
2	7298	99.9	1453	12	US-08-843-459-2
3	7287	99.8	1437	20	US-09-668-628-19
4	7297	99.8	1437	23	US-09-934-421A-6
5	7293	99.8	1437	1	PCT-US99-06644-4
6	4116	56.3	921	21	US-09-760-470-63
7	3037	41.6	1363	21	US-09-775-685-44

8	3016.5	41.3	1356	24	US-10-090-280-33	Sequence 33, Appl
9	3015	41.3	1359	24	US-10-090-280-34	Sequence 34, Appl
10	2916.5	39.9	1332	21	US-09-775-685-50	Sequence 50, Appl
11	2865	39.2	569	21	US-09-760-470-51	Sequence 51, Appl
12	2865	39.2	569	21	US-09-760-483-464	Sequence 464, App
13	2643.5	36.2	1331	20	US-09-668-628-1	Sequence 1, Appl
14	2637	36.1	1379	21	US-09-703-253-18	Sequence 18, Appl
15	2583.5	35.4	1216	21	US-09-775-685-46	Sequence 46, Appl
16	2563.5	35.1	1247	21	US-09-775-685-48	Sequence 48, Appl
17	2540.5	34.8	1360	23	US-09-934-421A-2	Sequence 2, Appl
18	2425	33.2	1077	26	US-60-299-484-36	Sequence 36, Appl
19	2401	32.9	1238	26	US-60-207-558-359	Sequence 359, App
20	2316.5	31.7	1216	21	US-09-703-253-24	Sequence 24, Appl
21	2290	31.3	1063	21	US-09-703-253-6	Sequence 6, Appl
22	2086	28.5	1545	26	US-60-333-700-44	Sequence 44, Appl
23	2086	28.5	1545	26	US-60-333-700-4	Sequence 4, Appl
24	2085	28.5	1545	26	US-60-333-700-24	Sequence 24, Appl
25	2085	28.5	1545	26	US-60-333-700-26	Sequence 26, Appl
26	2085	28.5	1545	26	US-60-333-700-28	Sequence 28, Appl
27	2085	28.5	1545	26	US-60-333-700-30	Sequence 30, Appl
28	2085	28.5	1545	26	US-60-333-700-32	Sequence 32, Appl
29	2085	28.5	1545	26	US-60-333-700-34	Sequence 34, Appl
30	2085	28.5	1545	26	US-60-333-700-40	Sequence 40, Appl
31	2085	28.5	1545	26	US-60-333-700-42	Sequence 42, Appl
32	2085	28.5	1545	26	US-60-333-700-46	Sequence 46, Appl
33	2085	28.5	1545	26	US-60-333-700-48	Sequence 48, Appl
34	2084	28.5	1545	26	US-60-333-700-38	Sequence 38, Appl
35	2082	28.5	1531	8	US-08-460-907A-4	Sequence 4, Appl
36	2082	28.5	1531	8	US-08-461-384A-4	Sequence 4, Appl
37	2082	28.5	1531	8	US-08-461-446A-4	Sequence 4, Appl
38	2082	28.5	1531	8	US-08-461-446B-4	Sequence 4, Appl
39	2082	28.5	1531	8	US-08-461-446C-4	Sequence 4, Appl
40	2082	28.5	1531	8	US-08-463-078A-4	Sequence 4, Appl
41	2082	28.5	1531	8	US-08-463-092A-4	Sequence 4, Appl
42	2082	28.5	1531	8	US-08-333-700-36	Sequence 36, Appl
43	2075	28.4	1531	6	US-08-292-309-8	Sequence 8, Appl
44	2075	28.4	1531	6	US-08-407-207-2	Sequence 2, Appl
45	2075	28.4	1531	8	US-08-460-907A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-528-031-2
Sequence 2, Application US/09528031
GENERAL INFORMATION:
APPLICANT: SHYJAN, Andrew
TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
POLYPEPTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,031
FILING DATE: 17-Mar-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-056CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ. ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-528-031-2

Query Match 100.0%; Score 7308; DB 19; Length 1437;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDIDGKTYIPSPGRSVRETSSTGTHREDSEKFRRTREPLECODALETARAGLS 60
 DB 1 MKDIDGKTYIPSPGRSVRETSSTGTHREDSEKFRRTREPLECODALETARAGLS 60
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 QY 121 VAHKKGELSMEDVWSLSKSHSSDVNCRRLERLMOEELNEVGPDAAISLRVWTFECPRLI 180
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 QY 241 AANTRTGVRRLGAILTMARKKILKLNKEKSLGELINCSNDGOMFEAAVAGSLIAG 300
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 DB 361 VETYEKFKMVAWKAFSQSVOKIREERRILKAGYFQSTIVGAPIVVIASVVTFSV 420
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 DB 421 HMTLGFDLTAQAFVTVFNSMTFALKVTPSVKSLASAVADRFSLFMEEVHMK 480
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 QY 541 VLAQKGLHLLDSDRSPREEEGKHILGHLRLQRTLHSLDLEIQEGKLVGICGSVSG 600
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 QY 841 VPMASVGYVIAAGGPLAFVIMALFNLVNGSTAFSTWMLSYNKKOSSGNTTYRGNETS 900
 DB 841 VPMASVGYVIAAGGPLAFVIMALFNLVNGSTAFSTWMLSYNKKOSSGNTTYRGNETS 900

DB 841 VPMASVGYVIAAGGPLAFVIMALFNLVNGSTAFSTWMLSYNKKOSSGNTTYRGNETS 900
 QY 901 VDSMKDNPQHOYYASTIALSMAVWLILKAIRGVFVNGTLRASSRLHDELFRRLRS 960
 DB 901 VDSMKDNPQHOYYASTIALSMAVWLILKAIRGVFVNGTLRASSRLHDELFRRLRS 960
 QY 961 KEFDTPTGRLNRFPSKMDVDVRLPQAMFQNVILVFCYGMILAGVPMFLVAVGP 1020
 DB 961 KEFDTPTGRLNRFPSKMDVDVRLPQAMFQNVILVFCYGMILAGVPMFLVAVGP 1020
 QY 1021 LVILFVSLHIVSRVILRELKRLDNITOSPFLSHITSSIOGLATHAANKGQEFHRYOEL 1080
 DB 1021 LVILFVSLHIVSRVILRELKRLDNITOSPFLSHITSSIOGLATHAANKGQEFHRYOEL 1080
 QY 1081 LDDQAPFFLFTCAMRLAARLDLISALTITTTGLMTVLNMGQIPPAVAGIASYAVOLT 1140
 DB 1081 LDDQAPFFLFTCAMRLAARLDLISALTITTTGLMTVLNMGQIPPAVAGIASYAVOLT 1140
 QY 1141 GLFOFTVRLASETARTSVBRINHYTKTSLAPPAIKKAPSPMPQGEVTFENAEM 1200
 DB 1141 GLFOFTVRLASETARTSVBRINHYTKTSLAPPAIKKAPSPMPQGEVTFENAEM 1200
 QY 1201 RYRENLPVLKVSFTIKPEKIGIVGRTSGKSSIGMALFRVLVELSGGCIKIDGVRISD 1260
 DB 1201 RYRENLPVLKVSFTIKPEKIGIVGRTSGKSSIGMALFRVLVELSGGCIKIDGVRISD 1260
 QY 1261 IGLADLRSKSTIPQEPVLFSGTVRSNLDPEFNOYTEDQIWDALERTHMKRCIAQLPLKLE 1320
 DB 1261 IGLADLRSKSTIPQEPVLFSGTVRSNLDPEFNOYTEDQIWDALERTHMKRCIAQLPLKLE 1320
 QY 1321 SEVENGDNEFSVEROLLICARALLRHCKILLIDEATAMPDPTDILLIQTETREATDCT 1380
 DB 1321 SEVENGDNEFSVEROLLICARALLRHCKILLIDEATAMPDPTDILLIQTETREATDCT 1380
 QY 1381 MLTIARLHTVLGSDRIWLAQGVVEFDTPSVLSSNDSRFYAMFAAENKVAAYG 1437
 DB 1381 MLTIARLHTVLGSDRIWLAQGVVEFDTPSVLSSNDSRFYAMFAAENKVAAYG 1437

RESULT 2
 US-08-843-459-2
 ; Sequence 2, Application US/08843459
 ; GENERAL INFORMATION:
 ; APPLICANT: SHYJAN, Andrew
 ; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
 ; TITLE OF INVENTION: POLYPEPTIDE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESS: Testa, Hurwitz & Thibault
 ; STREET: 125 High St.
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/843,459
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FENTON, Gillian M
 ; REGISTRATION NUMBER: 36,508
 ; REFERENCE/DOCKET NUMBER: MIL-001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 248-7100
 ; TELEFAX: (617) 248-7100
 ; INFORMATION FOR SEQ. ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1453 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-843-459-2

Query Match 99.9%; Score 7298; DB 12; Length 1453;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDIDGKEYIIPSPGRSVREKSTSGTHDRDSEKFRRTREPLECODALETAARAGLS 60
17 MKDIDGKEYIIPSPGRSVREKSTSGTHDRDSEKFRRTREPLECODALETAARAGLS 76
QY 61 LDASMSQRLILDEBHKGYHNGLSALKPRTTCKHQPVDNAGLFCSCMFSWLSLAR 120
77 LDASMSQRLILDEBHKGYHNGLSALKPRTTCKHQPVDNAGLFCSCMFSWLSLAR 136
QY 121 VAHKGELSMEDVWSLSKHESSDVNCRRLERLMOEELNEVGPDAAASLRVWVIFCRTL 180
137 VAHKGELSMEDVWSLSKHESSDVNCRRLERLMOEELNEVGPDAAASLRVWVIFCRTL 196
QY 181 LSTVCLMTQLAGSGPAFWKHLLEYTQATESNLQYSLLVGLLLEIVRSWLSALTW 240
197 LSTVCLMTQLAGSGPAFWKHLLEYTQATESNLQYSLLVGLLLEIVRSWLSALTW 256
QY 241 ALVYRPGVRLRGALITMAFKKILKRIKESLIGELINISNGQRFEEAAVAGSLLAG 300
257 ALVYRPGVRLRGALITMAFKKILKRIKESLIGELINISNGQRFEEAAVAGSLLAG 316
QY 301 PVVAIIIGMIVNIIIGPTGFLGSAVEILFEYPAMMFASRLTAYFRKCVAAATDERVOKME 360
317 PVVAIIIGMIVNIIIGPTGFLGSAVEILFEYPAMMFASRLTAYFRKCVAAATDERVOKME 376
QY 361 VLTYYIKFYAWVAKFSQSVOKIREERRILEKAGYFOSITVGVAPIVVAVSVTFESV 420
377 VLTYYIKFYAWVAKFSQSVOKIREERRILEKAGYFOSITVGVAPIVVAVSVTFESV 436
QY 421 HMTLGFDTLTAOAFVTVTVNSMTFALKTPYFVKSLSSEASVAVDRKSLFLMEVAMIK 480
437 HMTLGFDTLTAOAFVTVTVNSMTFALKTPYFVKSLSSEASVAVDRKSLFLMEVAMIK 496
QY 481 NKPSPHIKIEMKNATLAMDSSHSSTIONSPLTPPKMKKDRASRGKKEKROLORTEHOA 540
497 NKPSPHIKIEMKNATLAMDSSHSSTIONSPLTPPKMKKDRASRGKKEKROLORTEHOA 556
QY 541 VLAEGKGHLLDSDERSPEEKGKHLHGLRLQRTLSIDETIQGKLVGICGSVSG 600
557 VLAEGKGHLLDSDERSPEEKGKHLHGLRLQRTLSIDETIQGKLVGICGSVSG 616
QY 601 KTSLSIAIIGOMTLLEGSAISTGFAYVAQOAMTLNATLDNIIIFGKEYDEBERNSVLNS 660
617 KTSLSIAIIGOMTLLEGSAISTGFAYVAQOAMTLNATLDNIIIFGKEYDEBERNSVLNS 676
QY 661 CCLRPDLAIIIPSSDLTEIGERGAMLSGGQRISIAARALSDRSIYLLDPLSLDAHV 720
677 CCLRPDLAIIIPSSDLTEIGERGAMLSGGQRISIAARALSDRSIYLLDPLSLDAHV 736
QY 721 NHIFSAIRKHLKSKTVLFTVTHQLQYLVDCDEVIFMKEGCITERTGHEELMNLNGDYATI 780
737 NHIFSAIRKHLKSKTVLFTVTHQLQYLVDCDEVIFMKEGCITERTGHEELMNLNGDYATI 796
QY 781 FNNLLGEPFVPIVNSKKESSGSKSODKGPRTGSIKKRKAAYRREGOLVLEEKQGS 840
797 FNNLLGEPFVPIVNSKKESSGSKSODKGPRTGSIKKRKAAYRREGOLVLEEKQGS 856
QY 841 VPMISVGVYIOAGCPDLAFLVIALFMFLANGSTAFSTMWLSYMKOSGGTITVTRGETS 900
857 VPMISVGVYIOAGCPDLAFLVIALFMFLANGSTAFSTMWLSYMKOSGGTITVTRGETS 916
QY 901 VSDSMKDNPMOYIYASTIYALSMVMLLKAIRGVVGVKGLTLRASSRLDELFRILLSPM 960
917 VSDSMKDNPMOYIYASTIYALSMVMLLKAIRGVVGVKGLTLRASSRLDELFRILLSPM 976

QY 961 KFFDTTPGRILNRESKMDDEVDRLPFOAEMFIONVILVEFCYGMAGVPMFLVAVGP 1020
977 KFFDTTPGRILNRESKMDDEVDRLPFOAEMFIONVILVEFCYGMAGVPMFLVAVGP 1036
QY 1021 LVILFVSLHIVSRVILRELKRLDNITOSPFLSHITSSIOGLATITHAANKGOEFLHRYOEL 1080
1037 LVILFVSLHIVSRVILRELKRLDNITOSPFLSHITSSIOGLATITHAANKGOEFLHRYOEL 1096
QY 1081 LDDNQAPPEFLTCAMRWLAVLDLISALTITTTGMLYLMHGOIPRAYAGIAISAVOLT 1140
1097 LDDNQAPPEFLTCAMRWLAVLDLISALTITTTGMLYLMHGOIPRAYAGIAISAVOLT 1156
QY 1141 GLFOFVRLASETEARFVSIRINHYITKTSLEAPARKKAPSPDMPDQBEVFPENEM 1200
1157 GLFOFVRLASETEARFVSIRINHYITKTSLEAPARKKAPSPDMPDQBEVFPENEM 1216
QY 1201 RYRENPLVLKRVSFITPKKEIGIVRTGSGKSLGMAFLRVELSGGCIKIDGVRTSD 1260
1217 RYRENPLVLKRVSFITPKKEIGIVRTGSGKSLGMAFLRVELSGGCIKIDGVRTSD 1276
QY 1261 IGLADLRKSLIIPQEPVLSGTVRSNLDPEPNOYTEDQIMDALERTHMKECIAOLPLKLE 1320
1277 IGLADLRKSLIIPQEPVLSGTVRSNLDPEPNOYTEDQIMDALERTHMKECIAOLPLKLE 1336
QY 1321 SEVENMGDNPSVGEROLCTARALLRHCKILLDEATRAMTEPDLIOETIREAFADCT 1380
1337 SEVENMGDNPSVGEROLCTARALLRHCKILLDEATRAMTEPDLIOETIREAFADCT 1396
QY 1381 MLTIAHRLHVLVGSDRIMVLAQGVFERPVSLSNDSRFYAMFAAEKKAHVAKG 1437
1397 MLTIAHRLHVLVGSDRIMVLAQGVFERPVSLSNDSRFYAMFAAEKKAHVAKG 1453

RESULT 3
US-09-668-628-19
Sequence 19, Application us/09668628
GENERAL INFORMATION:
APPLICANT: Krasnow, Randi E.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: ATP-BINDING CASSETTE PROTEIN
FILE REFERENCE: PC-0021 US
CURRENT APPLICATION NUMBER: us/09/668, 628
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PERL Program
SEQ ID NO 19
LENGTH: 1437
TYPE: PRP
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: g5605864
US-09-668-628-19

Query Match 99.8%; Score 7297; DB 20; Length 1437;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1435; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKDIDGKEYIIPSPGRSVREKSTSGTHDRDSEKFRRTREPLECODALETAARAGLS 60
1 MKDIDGKEYIIPSPGRSVREKSTSGTHDRDSEKFRRTREPLECODALETAARAGLS 60
QY 61 LDASMSQRLILDEBHKGYHNGLSALKPRTTCKHQPVDNAGLFCSCMFSWLSLAR 120
61 LDASMSQRLILDEBHKGYHNGLSALKPRTTCKHQPVDNAGLFCSCMFSWLSLAR 120
QY 121 VAHKGELSMEDVWSLSKHESSDVNCRRLERLMOEELNEVGPDAAASLRVWVIFCRTL 180
121 VAHKGELSMEDVWSLSKHESSDVNCRRLERLMOEELNEVGPDAAASLRVWVIFCRTL 180
QY 181 LSTVCLMTQLAGSGPAFWKHLLEYTQATESNLQYSLLVGLLLEIVRSWLSALTW 240

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181 LSIIVCMITQLAGFSGPAPVWKHLLEYQATESNLQYSLLVGLLLEIVRSMLALTW 240
241 ALNRYTGVRLRGAILTMARKKILTKNIKEKSTIGELINICSDGOMFEAANGSLLAG 300
241 ALNRYTGVRLRGAILTMARKKILTKNIKEKSTIGELINICSDGOMFEAANGSLLAG 300
301 PVVAILGMIYNYIILGPTGFLGSAVFIIFYPAMFASRLTAYFRRCVATDERVOKNE 360
301 PVVAILGMIYNYIILGPTGFLGSAVFIIFYPAMFASRLTAYFRRCVATDERVOKNE 360
361 VLTITKFTKMYAMVAFKFSQVOKIREERRILEKAGYFOSITVGAPIVVIVASVTFV 420
361 VLTITKFTKMYAMVAFKFSQVOKIREERRILEKAGYFOSITVGAPIVVIVASVTFV 420
421 HMTLGFDLTAQAQAFVTVVFNSTFALKVTPSVKSLSEASVAVDFKSLFLEEVHMK 480
421 HMTLGFDLTAQAQAFVTVVFNSTFALKVTPSVKSLSEASVAVDFKSLFLEEVHMK 480
481 NKPSAPHIKIEMKNATLAMDSSHSIIONSPKLTPEKMKKDRASRGKKEVROLQTEHOA 540
481 NKPSAPHIKIEMKNATLAMDSSHSIIONSPKLTPEKMKKDRASRGKKEVROLQTEHOA 540
541 VLABOKGHLLDSDERPEEPEGKHILGHLRLQRTLSIDLEIOEGKLVGICGSVSG 600
541 VLABOKGHLLDSDERPEEPEGKHILGHLRLQRTLSIDLEIOEGKLVGICGSVSG 600
601 KTSLSAIIIGOMTLEGSAISGTFAVYAOAMILNATRLDNTLREKEDDEREYNSVLNS 660
601 KTSLSAIIIGOMTLEGSAISGTFAVYAOAMILNATRLDNTLREKEDDEREYNSVLNS 660
661 CCLRPDLALPSSDLTEIGERGANSOGORQRIISALARYSDRIYIILDDPLSALDAHG 720
661 CCLRPDLALPSSDLTEIGERGANSOGORQRIISALARYSDRIYIILDDPLSALDAHG 720
721 NHIEVSARKHUKSTVLFVTHOLOLVDCDEVITNKESCTERGTHEEMLMNGDYATI 780
721 NHIEVSARKHUKSTVLFVTHOLOLVDCDEVITNKESCTERGTHEEMLMNGDYATI 780
781 FNNLLGEPPEINSKETSOGSKSODKGPKTGSIKKERVKPEEGOLVLEEGGSS 840
781 FNNLLGEPPEINSKETSOGSKSODKGPKTGSIKKERVKPEEGOLVLEEGGSS 840
841 VPMVYGYVIOAAGGPLAFVLMALFNLVNGSTAFSTWMLSYWIKOGSNTVTGNETS 900
841 VPMVYGYVIOAAGGPLAFVLMALFNLVNGSTAFSTWMLSYWIKOGSNTVTGNETS 900
901 VSDSKDNPDMOYVASTYALSMAVWLILKALRGVVFVKGTLRASSRLHDELFRILRSPM 960
901 VSDSKDNPDMOYVASTYALSMAVWLILKALRGVVFVKGTLRASSRLHDELFRILRSPM 960
961 KEFDTPTGRILNRPESKMDVDVRLPROAEMFIONVILVFCVGMIAGVFPWFLVANGP 1020
961 KEFDTPTGRILNRPESKMDVDVRLPROAEMFIONVILVFCVGMIAGVFPWFLVANGP 1020
1021 LVILFVLAHVSRLIRELRLDNTQSPFLSHITSSIOGLATTHAYNKGOFELRYOEL 1080
1021 LVILFVLAHVSRLIRELRLDNTQSPFLSHITSSIOGLATTHAYNKGOFELRYOEL 1080
1081 LDNDQAPPEFLTCAMRWLAVALDLISALITTTGLMIVLMHQIIPPAYAGLAISYAVOLT 1140
1081 LDNDQAPPEFLTCAMRWLAVALDLISALITTTGLMIVLMHQIIPPAYAGLAISYAVOLT 1140
1141 GLPQFTYRLASETARFVSERINHYITLSLEAPARKKNAKPSDWMQEGEVTFENAM 1200
1141 GLPQFTYRLASETARFVSERINHYITLSLEAPARKKNAKPSDWMQEGEVTFENAM 1200
1201 RYRENBLVLAKVYFTIKPKKIGIVGTGSGKSSIGMALRLVELSGGCIKIDVVRISD 1260
1201 RYRENBLVLAKVYFTIKPKKIGIVGTGSGKSSIGMALRLVELSGGCIKIDVVRISD 1260
1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPEFNOYTEQIMDALEKTHKECIAQLPLE 1320
1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPEFNOYTEQIMDALEKTHKECIAQLPLE 1320

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1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPEFNOYTEQIMDALEKTHKECIAQLPLE 1320
1321 SEVWENDNFSVGBRQLCTARALLRHCKLILIDEATAAMDTEDDLIOETIREAFADCT 1380
1321 SEVWENDNFSVGBRQLCTARALLRHCKLILIDEATAAMDTEDDLIOETIREAFADCT 1380
1381 MLTIAHLHTVLGSDRLMVLVAGOVVEFDPFVSLLSSDRFAMFAAANKVAVKG 1437
1381 MLTIAHLHTVLGSDRLMVLVAGOVVEFDPFVSLLSSDRFAMFAAANKVAVKG 1437

RESULT 4
US-09-934-421A-6
; Sequence 6: Application US/09934421A
; GENERAL INFORMATION:
; APPLICANT: Curtis, RORY A. J.
; TITLE OF INVENTION: 44589, A NOVEL HUMAN ABC TRANSPORTER
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-083001
; CURRENT APPLICATION NUMBER: US/09/934,421A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/226,770
; PRIOR FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1437
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-934-421A-6

Query Match 99.8%; Score 7297; DB 23; Length 1437;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1435; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MKDIDIGKEIYIPSPGRSVRERTSTSGTHRODESKFRTTRPLECODALETAAREGIS 60
1 MKDIDIGKEIYIPSPGRSVRERTSTSGTHRODESKFRTTRPLECODALETAAREGIS 60
61 LDASHMSQRLIDEHPKRYHNGLSALKPRTTCKHQHPVDNAGLFSQMTFSWLSLAR 120
61 LDASHMSQRLIDEHPKRYHNGLSALKPRTTCKHQHPVDNAGLFSQMTFSWLSLAR 120
121 VAHKGELSMEVWSISKHSSDVNCRLERLMOEFLNEVGDPAASLRVWVIFCRTL 180
121 VAHKGELSMEVWSISKHSSDVNCRLERLMOEFLNEVGDPAASLRVWVIFCRTL 180
181 LSIIVCMITQLAGFSGPAPVWKHLLEYQATESNLQYSLLVGLLLEIVRSMLALTW 240
181 LSIIVCMITQLAGFSGPAPVWKHLLEYQATESNLQYSLLVGLLLEIVRSMLALTW 240
241 ALNRYTGVRLRGAILTMARKKILTKNIKEKSTIGELINICSDGOMFEAANGSLLAG 300
241 ALNRYTGVRLRGAILTMARKKILTKNIKEKSTIGELINICSDGOMFEAANGSLLAG 300
301 PVVAILGMIYNYIILGPTGFLGSAVFIIFYPAMFASRLTAYFRRCVATDERVOKNE 360
301 PVVAILGMIYNYIILGPTGFLGSAVFIIFYPAMFASRLTAYFRRCVATDERVOKNE 360
361 VLTITKFTKMYAMVAFKFSQVOKIREERRILEKAGYFOSITVGAPIVVIVASVTFV 420
361 VLTITKFTKMYAMVAFKFSQVOKIREERRILEKAGYFOSITVGAPIVVIVASVTFV 420
421 HMTLGFDLTAQAQAFVTVVFNSTFALKVTPSVKSLSEASVAVDFKSLFLEEVHMK 480
421 HMTLGFDLTAQAQAFVTVVFNSTFALKVTPSVKSLSEASVAVDFKSLFLEEVHMK 480
481 NKPSAPHIKIEMKNATLAMDSSHSIIONSPKLTPEKMKKDRASRGKKEVROLQTEHOA 540
481 NKPSAPHIKIEMKNATLAMDSSHSIIONSPKLTPEKMKKDRASRGKKEVROLQTEHOA 540
541 VLABOKGHLLDSDERPEEPEGKHILGHLRLQRTLSIDLEIOEGKLVGICGSVSG 600
541 VLABOKGHLLDSDERPEEPEGKHILGHLRLQRTLSIDLEIOEGKLVGICGSVSG 600

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Db 541 VLAEOKGHLLDSDRSPPEEEKGHIHGLRLQRTLHSDLEEOGLVIGCSVSG 600
Qy 601 KTSLSAILGOMTLLEGSAISGTFAYVAQOAMILNATLRDNIIFGKEDEERYNSVLS 660
Db 601 KTSLSAILGOMTLLEGSAISGTFAYVAQOAMILNATLRDNIIFGKEDEERYNSVLS 660
Qy 661 CCLRPDLALPSSDLTEIGERGANLGGORORISLARALYSRSTIYIIDPLSALDAHVG 720
Db 661 CCLRPDLALPSSDLTEIGERGANLGGORORISLARALYSRSTIYIIDPLSALDAHVG 720
Qy 721 NHIFSAIRKHLKSKTVLFVTHQLOYLVDCDEVIFMKEGCTIERGTHELMNLNGDYATI 780
Db 721 NHIFSAIRKHLKSKTVLFVTHQLOYLVDCDEVIFMKEGCTIERGTHELMNLNGDYATI 780
Qy 781 FNNLLGTPPEVINSKETSQSKSODKPGKTSIKKEKAVKPEEGOLVLEEKGGGS 840
Db 781 FNNLLGTPPEVINSKETSQSKSODKPGKTSIKKEKAVKPEEGOLVLEEKGGGS 840
Qy 841 VPMSYGYVIOAGGPLAFVIMALFMLNVSSTAFSTMWLSWIKOGSGNTTVTRGNETS 900
Db 841 VPMSYGYVIOAGGPLAFVIMALFMLNVSSTAFSTMWLSWIKOGSGNTTVTRGNETS 900
Qy 901 VSDSKNDPNQYAYASIVALSMAVWLILKAIKGVVFKGTLRASSRLHDELFRILRSPM 960
Db 901 VSDSKNDPNQYAYASIVALSMAVWLILKAIKGVVFKGTLRASSRLHDELFRILRSPM 960
Qy 961 KEFTTTPGRLINRFSKMDVDVRLPQOAEFIONVILVFFCVMIAGVPEMELVAVGP 1020
Db 961 KEFTTTPGRLINRFSKMDVDVRLPQOAEFIONVILVFFCVMIAGVPEMELVAVGP 1020
Qy 1021 LVILFVSLHVSRLIRELRLDNTOSPFLSHITSSIOGLAT HAYKKGOFELHRYOL 1080
Db 1021 LVILFVSLHVSRLIRELRLDNTOSPFLSHITSSIOGLAT HAYKKGOFELHRYOL 1080
Qy 1081 LDDNOAPEFLFTCAMRWLAVRLDLISALITTTGLMIVLMHQIPPAAGLAISVAVOLT 1140
Db 1081 LDDNOAPEFLFTCAMRWLAVRLDLISALITTTGLMIVLMHQIPPAAGLAISVAVOLT 1140
Qy 1141 GLFOFYRLASETARFISVRINHYITLSEAPARKKAPSDWQEGEVTFENAM 1200
Db 1141 GLFOFYRLASETARFISVRINHYITLSEAPARKKAPSDWQEGEVTFENAM 1200
Qy 1201 RYRENLPVLKVSFTTIKPKKIGIVRTGSGKSLGALFRLVLSGGCIKIDSVRISD 1260
Db 1201 RYRENLPVLKVSFTTIKPKKIGIVRTGSGKSLGALFRLVLSGGCIKIDSVRISD 1260
Qy 1261 IGLADLRKSLIIPQEPVLFSGTVRSNLPNOQTEDQIMDALERTHMKECIAQLPLKLE 1320
Db 1261 IGLADLRKSLIIPQEPVLFSGTVRSNLPNOQTEDQIMDALERTHMKECIAQLPLKLE 1320
Qy 1321 SEVENNDNFVGEROLLICIRALLRHCKIILDEBATAAMTETDILLOETIREAFADCT 1380
Db 1321 SEVENNDNFVGEROLLICIRALLRHCKIILDEBATAAMTETDILLOETIREAFADCT 1380
Qy 1381 MLTIAHRLHTVLSGDRIMVLAOGOVVERDPVSILSNDSPRYAMEAAENKVAVKG 1437
Db 1381 MLTIAHRLHTVLSGDRIMVLAOGOVVERDPVSILSNDSPRYAMEAAENKVAVKG 1437

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RESULT 5
PCT-US99-06644-4
; Sequence 4, Application PC/TUS9906644
; GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruh, Gary D.
; APPLICANT: Lee, Kun
; APPLICANT: Belinsky, Martin G.
; APPLICANT: Bain, Lisa J.
; TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
; FILE REFERENCE: FCCC 98-02
; CURRENT APPLICATION NUMBER: PCT/US99/06644

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; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/079,759
; EARLIER FILING DATE: 1998-03-27
; EARLIER APPLICATION NUMBER: 60/095,153
; EARLIER FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 4
; LENGTH: 1437
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US99-06644-4

Query Match 99.8%; Score 7293; DB 1; Length 1437;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1434; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKDIDIGKEYIIPSPGYRVSRETSSTGTHRDREDSKFRRTPLRLECODALETAARAEGLS 60
Db 1 MKDIDIGKEYIIPSPGYRVSRETSSTGTHRDREDSKFRRTPLRLECODALETAARAEGLS 60
Qy 61 IDASHMSQRLIDEEHPKGYHHGLSALKPIRTTCKHQHPVDNAGLFSCTPESWLSLAR 120
Db 61 IDASHMSQRLIDEEHPKGYHHGLSALKPIRTTCKHQHPVDNAGLFSCTPESWLSLAR 120
Qy 121 VAHKGELSMEDVWSLSKHESSDVNCRRLERLMOEELNVEYGDASLRVYVWIFCETRLI 180
Db 121 VAHKGELSMEDVWSLSKHESSDVNCRRLERLMOEELNVEYGDASLRVYVWIFCETRLI 180
Qy 181 ISTVCLMTIOLAGFSGPAPMVKHLELYQATESNLQYSLVLVGLLTFEIVSMSLATM 240
Db 181 ISTVCLMTIOLAGFSGPAPMVKHLELYQATESNLQYSLVLVGLLTFEIVSMSLATM 240
Qy 241 ALNVRTGVRGAILTMAFKILKLNKESLGEILINICSDNGORMEPAAVGSLLAG 300
Db 241 ALNVRTGVRGAILTMAFKILKLNKESLGEILINICSDNGORMEPAAVGSLLAG 300
Qy 301 PVVAILGMIVNYIILGPGFELGSANVILFYPAMPFASRLTAYFRRCVCAATDERVQKME 360
Db 301 PVVAILGMIVNYIILGPGFELGSANVILFYPAMPFASRLTAYFRRCVCAATDERVQKME 360
Qy 361 VTYIYKFTIMVAVKAFSOSVOKIRREERIRILEKGYFOSIVGVAPIVYVIVASVYTFSV 420
Db 361 VTYIYKFTIMVAVKAFSOSVOKIRREERIRILEKGYFOSIVGVAPIVYVIVASVYTFSV 420
Qy 421 HMTLGFDLTAAQAFVTVYFNSMTFALKVTPSVKSLSEASVAVDRFKSLFLMEEVHMK 480
Db 421 HMTLGFDLTAAQAFVTVYFNSMTFALKVTPSVKSLSEASVAVDRFKSLFLMEEVHMK 480
Qy 481 NKPSAPHIKIEKKNATLAMDSSHSIIONSPKILTPMKKRRASRGKKEKVEVROLQRTHEHA 540
Db 481 NKPSAPHIKIEKKNATLAMDSSHSIIONSPKILTPMKKRRASRGKKEKVEVROLQRTHEHA 540
Qy 541 VLAEOKGHLLDSDRSPPEEEKGHIHGLRLQRTLHSDLEEOGLVIGCSVSG 600
Db 541 VLAEOKGHLLDSDRSPPEEEKGHIHGLRLQRTLHSDLEEOGLVIGCSVSG 600
Qy 601 KTSLSAILGOMTLLEGSAISGTFAYVAQOAMILNATLRDNIIFGKEDEERYNSVLS 660
Db 601 KTSLSAILGOMTLLEGSAISGTFAYVAQOAMILNATLRDNIIFGKEDEERYNSVLS 660
Qy 661 CCLRPDLALPSSDLTEIGERGANLGGORORISLARALYSRSTIYIIDPLSALDAHVG 720
Db 661 CCLRPDLALPSSDLTEIGERGANLGGORORISLARALYSRSTIYIIDPLSALDAHVG 720
Qy 721 NHIFSAIRKHLKSKTVLFVTHQLOYLVDCDEVIFMKEGCTIERGTHELMNLNGDYATI 780
Db 721 NHIFSAIRKHLKSKTVLFVTHQLOYLVDCDEVIFMKEGCTIERGTHELMNLNGDYATI 780
Qy 781 FNNLLGTPPEVINSKETSQSKSODKPGKTSIKKEKAVKPEEGOLVLEEKGGGS 840
Db 781 FNNLLGTPPEVINSKETSQSKSODKPGKTSIKKEKAVKPEEGOLVLEEKGGGS 840

```


SEQ ID NO 44
LENGTH: 1363
TYPE: PRN
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(1363)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-775-685-44

Query Match 41.6%; Score 3037; DB 21; Length 1363;
Best Local Similarity 45.3%; Pred. No. 2e-273;
Matches 621; Conservative 254; Mismatches 441; Indels 56; Gaps 14;

80 KYHHGSLALPRTTCK-HQHPVDNAGLFCSCMTFMSLSLARVAHKKGELSMEDVMSLK 138
24 RYDPSLKTMTIPVPCARLAPNVPDAGLLSFATFSWLTPLVMVKGVRQ-RLTVDTLPPLST 82
139 HESSDVNCRRLERLMOBELNEVGPDASLRVWVIFCRTLILSYVCLMTOLAGFSGPA 198
83 YDSDTNNAKFRVLMDEVARVGPBKASLSHVWKKFORIVLMDIVANILCTIIMAAIGPT 142
199 FVVKHLELYQATESNLQYSLILVGLLLEIYRSWSLALTMALNTGYRLKGAITMA 258
143 VLIHQILOOTERTSGKWVIGICLALFATEFTRVFWMALAMAINVTAIRKVALSTLV 202
259 FKILKLNKESLGLINICSDGOMFEAAGVSLAGPVAIVLGMVYIIGPT 318
203 FEMVSKTLTHISVGVNLISDSYSLEFALFCLPLPATIPLMFECAAYAFIIGPT 262
319 GFPSAFLIFYPAMFASRLTAFERRKCYAATDEROYKNEVITYIKFKIMAMVKAFS 378
263 ALIGISYVLFIVQMFALNSFRSALVTDKRVOTNNEFTICRLIKMAWESFT 322
379 QSVOKITREERRILKAKGPOSITVGVPIVIVYASVVFESVMTLGLFDLTAQAFTVVT 438
323 INTIODIRRRERKLEKAGFVQSGNSALAPIVSTAIYVLTLSCHILLRKLLAPAVAFVIA 382
439 VFNSTPALKVTPSVKSLSEASVANDRFSLFMEVNHAKKPAIPHIEKKNATLA 498
383 MFVNMKESIALPFSIKAAEAVNSLRMRKILDKSPSYTIQPEPDVYLLANATLT 442
499 WDSHSSISQPKLTPKMKDKRASRGKEKVRQLQTEHQAVLAEOKGHLLDSDRPS 558
443 WEH-----EASRSTPKLONOKRHCLKKORSEAYSERSPA-----KG-----ATG 484
559 PEEBEGKHILGHLRLQRTLSIDLEIOEKLVGICGVSQKSLISAILGQMTLEGS 618
485 PEGSDS-----LKSVLHSISFVVRKGIIGICGVSGSKSLAALLGQMOLOKV 536
619 IALSGTAYVAQAMINATLRDNLFGKEYDEBRVNSVLSCLRPDLAILPSSDLET 678
537 VAANGTLAYVSOQAMIFHGVRNILEGKEYDHOHTVRVCGILOKDLNLPYGDLEI 596
679 GEGGANLSGGORISARALYSRSLYIIDDPLSALDAVGNHIFNSAIRKHKSKTVL 738
597 GEGNLSGGORISARALYSRSLYIIDDPLSALDAVGNHIFNSAIRKHKSKTVL 738
739 FVTHOLOLVDCDEVIFMKKCTTERTGTHELMNLNGVATIFNNL--LIGETP----- 790
657 LVTHOLOLVDCDEVIFMKKCTTERTGTHELMNLNGVATIFNNL--LIGETP----- 790
791 -----PVEINSKKETSGSOKSODKPKPGSIRKEKAVPREGOLVLEEGOGSV 841
717 AMVEAFKESPAEEDAVLAPGNEKGEKSEETGS--EFVDTKPEHQLQTESPQGT 774
842 PMSVGYIQAAGPLAFILMALFMLNVTAFSTFWLVSVMKOGSGNTVTRGNT-- 899
775 TMTIYHYIKASGGYLSLSTVFLFLMTIGSAASNMWLGIMDKGRMTCGPGNRTWC 834
900 SVDSMKD-NPHQYVASIYALSMAVLLIKAIRGVVFGVGLTASRLDELFRRLRS 958

835 EVGAVLADIGQHV--YQWVYASVFMVLFVGVTKGFEVFTKTLTMASSSLHDVFDKILKS 892
959 PMKFEOTTPGRIINRSKMDVDVLPFOAEFIONVILFPCVMIAGVFWPLVAV 1018
893 PMSEFDTTPGRILNRSKMDDELVDRLPFAENFLOQFFWVFIILVLAAPVAVLLV 952
1019 GPVILFESVILSRVILREIKRLDNTQSPFSLTSSIOGLTALHAYNKGEFLHRYQ 1078
953 ASLAVGFILLRIFHRVQELKAVENSRSPWFHITSSMOGLIITAYKKESCI---T 1009
1079 ELDDNQAPFELFCAMRLAVRLDLISALITTTGIMVLMHGOIPPAVAGLAISYVQ 1138
1010 TLNDENSHLLYFNCALRWFALRMDVLMNITFTVALLVTLFSFISSTSGSLSTYII 1069
1139 LTGIFQTVPLASTERTKFTSVKINRYITLSLEAPARKKNAKPSDMQDEGVTEMA 1198
1070 LSGILOCVRTGETQAKFISVLELRYSITCVCECHNPLKVGTCPPDWSXGERTRDY 1129
1199 EMRYRENPLVLLKVSFTTIRKKEIGIVGRSGKSSLGMAFLVLESGCIRIDGVR 1258
1130 QMRKQNTPLVLDLSNLNINIOSGTVIGTRGSKSSLGMAFLVLESGCIRIDGVR 1189
1259 SDIGLADLRKSLIIPQEPVLFSGTVSNLDPFNQYTEDOIMALETHHKECTIAQLPLK 1318
1190 CILSLEDLRTKLVYIPQDPVLEVGTVRYNLDPFESHTEMLMOVLETFMRDITMKLPEK 1249
1319 LSEVMEGDNFSGEQOLLCIARALLRCKILLDATAAMTETDLLOETIREFAD 1378
1250 LQAEVTNGENFSGEQOLLCIARALLRCKILLDATAAMTETDLLOETIREFAD 1309
1379 CTMTIHRRLHTVYGSRIWLAQGVYFEDTPSVLSNDSRPYEAFAAE 1430
1310 CTYLTIAHRLNTVYLCNDHVLVMEKGVIEFDKPEVLAEKEDSAF-ANLLAAE 1360

RESULT 8
US-10-090-280-33
Sequence 33, Application us/10090280
GENERAL INFORMATION:
APPLICANT: AVENIS PHARMA SA
TITLE OF INVENTION: THE GOVERNMENT OF THE UNITED STATES,
TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABC12 GENE, VECTORS
FILE REFERENCE: ABC12 GENE
CURRENT APPLICATION NUMBER: US/10/090, 280
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: 60/272,759
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 1356
TYPE: PRN
ORGANISM: Homo sapiens
US-10-090-280-33

Query Match 41.3%; Score 3016.5; DB 24; Length 1356;
Best Local Similarity 45.0%; Pred. No. 1.6e-271;
Matches 618; Conservative 253; Mismatches 438; Indels 63; Gaps 14;

80 KYHHGSLALPRTTCK-HQHPVDNAGLFCSCMTFMSLSLARVAHKKGELSMEDVMSLK 138
24 RYDPSLKTMTIPVPCARLAPNVPDAGLLSFATFSWLTPLVMVKGVRQ-RLTVDTLPPLST 82
139 HESSDVNCRRLERLMOBELNEVGPDASLRVWVIFCRTLILSYVCLMTOLAGFSGPA 198
83 YDSDTNNAKFRVLMDEVARVGPBKASLSHVWKKFORIVLMDIVANILCTIIMAAIGPT 142
199 FVVKHLELYQATESNLQYSLILVGLLLEIYRSWSLALTMALNTGYRLKGAITMA 258
143 VLIHQILOOTERTSGKWVIGICLALFATEFTRVFWMALAMAINVTAIRKVALSTLV 202

QY 259 FKKLIKNIKEKSGELINICSDGOMFEAAVGSLLAGGPVALLGMIYNIIGPT 318
 Db 203 FENLVSEKTLTHISVGEVLNLTSSDYSLEFEALFCPLPATIPILMWCAAYAFIIGPT 262
 QY 319 GFLGSAVFIIFYPAMMPASRLTAYFRKRCVAATDERVOKMNEVLTITKFIKIMYAVKAFS 378
 Db 263 ALIGISYVIFIPVQMPAKINSAFRRSAILVTDKRVQTMNEFLTCTIRLIKIMYAKESFT 322
 QY 379 OSVOKIREERERILEKAGYFOSITVGVAPIVVIVIASVVTESVHMTLGFEDLTAQAFTVVT 438
 Db 323 NTIODIRREERKLEKAGFVQSGNSALAPIVSTIAIVLTISCHILLRKLTAAPAFAFSVIA 382
 QY 439 VFNMTFALKVTPRSVVSLSASAVADVRFKSLFMEVEYHMKNNPASPBIKIEKNATLA 498
 Db 383 MFNNMKFSIALLPFSIKAMAEANVSLRMRKILLDKSPSYITQPEPBDVLLANATLT 442
 QY 499 WDSHSSIONSPLTPMKKDKRASRGKKEKRVOLQRTHOAVLAEOKGHLLDSDERS 558
 Db 443 WEH-----EASRKSTPKKLQKOKRHCLKORSEAYSERSPA-----KG-----ATG 484
 QY 559 PEEBEGKHILGHLRLOTHSIDLEIOEKLVGICGSVSGKTSLSAIIAGMTLEGS 618
 Db 485 PEEQSDS-----LKSVLHSISFVVRKGIIGICGVSGKSSLLAALGQOLQGV 536
 QY 619 IAIISGTAYVAQOAMILNATLRDNLIFGKEYDERYNSVLSCLRPDLALPSSDLEI 678
 Db 537 VAVNGTLAYVQOAMIFHGNVRNLIIFGEKDHQRYOHTYAVCGLOKDLNLPYGDLEI 596
 QY 679 GERGANLGGORORISLARALYSRSIYILDDPLSALDAVHNIIFNSAIKHLKSTVL 738
 Db 597 GERBLNLSGGORORISLARAVYSDROLXLDPLSAVDANAGKAVFECEIKTLRGKTV 656
 QY 739 FVTHQLOYLVDDEVIFEMKECCITERGTHERLNLNGDYATIFNLT--LIGETP----- 790
 Db 657 LVTHQLOFLESCDRAVILLEDEICEKGTNKLMEERGRYALINHLGLOKDEPHLYNA 716
 QY 791 -----PVEINSKETSGSOKKQDKGPKTGSIKKEKAVKPEEQVOLBEKGGSV 841
 Db 717 AMVEAFESPEREDAVLAPGNEKDEKESETS--EVDVTKVPEHQLQTESPORETV 774
 QY 842 PMASYGVYIOAGPLAFVILMALFNLVNGSTAFSTWMLSWIKOGSNTFVTGNET-- 899
 Db 775 TWKTYHYIRKASGYLSLFLVFLFLMIGSAFSNMMLGMLDKGSRMTCGPOGNRMK 834
 QY 900 SVSDSMKD-NPHMOYASTALSMANMLILKAIKGVVVFVKGTLLASRLHDELRILLRS 958
 Db 835 EVGAVLADIGOH--YQMVYTAAMVPMFLFEGVTKGFEVTKTTEMASSSLHDTVPDKILKS 892
 QY 959 PMKFEPTTPGRIINRSKMDDEVDRLPQAEFMFIONVILFFCVGAGVFPWFLVAV 1018
 Db 893 PMSEFDTTPGRIINRSKMDDELDRLPFAENFLOOFEMVAVFVLVLAVFAVAVLLV 952
 QY 1019 GFLVILSVLHIVSRVILRELKRLDNITQSPFLSHITSSIGLATIHAYNGOEFILHYQ 1078
 Db 953 ASLAVGEFILLIRHRCVQELKAYENSRSPWPHITSSMOGLGIIHAYGKKECITYH- 1011
 QY 1079 ELDDNOAPEFLFCAMRWLAIVLDLISALITTTGMLIVMHQOIPRAYGLAISTAVQ 1138
 Db 1012 -----LLYFNCALRMFWLIRMDVLMNLTFTVALVLTLSFSSISSTSGSLSTYIQ 1062
 QY 1139 LITGLFOFTVRLASFEARFTSVERIINHYIKTLSLEAPARIKNKAPSPDMPQEGEYTFNA 1198
 Db 1063 LSLGLQCVRGTEQOAFSTVSELLREYISTCVPECTHPLVGTCPKMPSCGETTFEDY 1122
 QY 1199 EMRYREMLPLVLRKVSFTIKRKIGIYGRGSGKSSLGMLFRLVELSGCIRKIDVRI 1258
 Db 1123 QMRKMDTPVLVDNLNLTQSGOYVIGRGSGKSSLGMLFRLVERASTITIDEVDI 1182
 QY 1259 SDGLADRSKLSIIPQEPVLSGTVRSNDLPENQYTEDQIMDALERTHMEKCTAQLPLK 1318
 Db 1183 CILSLEDLRTKLTVIPQDPVLFVGTVRYNLDPFESHTEMLMOVLERTFMDTJMKLPK 1242
 QY 1319 LEESEVMENGDMFVGEQRLLCICARALLRCKIILIDEATAMDMETDILLIOETREAPAD 1378

Db 1243 LQAEYENGEMFVGEQRLLCICARALLRNSKIILIDDATASMSKTTIYQNTIKDAFKG 1302
 QY 1379 CTMTLTAHRLTAVGSDRIWYLAQGYVEDTPSVLLSNDSPRYAMFAAE 1430
 Db 1303 CTVTIAHRLTAVLNCBHVLMENGKVTIEFDKPEVLAEKPDASAF-AMLLAAE 1353
 RESULT 9
 US-10-090-280-34
 ; Sequence 34, Application US/10090280
 ; GENERAL INFORMATION:
 ; APPLICANT: AVENTIS PHARMA SA
 ; APPLICANT: THE GOVERNMENT OF THE UNITED STATES,
 ; TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABC12 GENE, VECTORS
 ; FILE REFERENCE: CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF
 ; CURRENT APPLICATION NUMBER: US/10/090,280
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 60/272,759
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 34
 ; LENGTH: 1359
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-090-280-34
 Query Match 41.3% Score 3015; DB 24; Length 1359;
 Best Local Similarity 44.8%; Pred. No. 2.3e-271;
 Matches 618; Conservative 255; Mismatches 432; Indels 74; Gaps 15;
 QY 80 KUNHGSALKPIRTCK-HQHPVONAGLFCGMPFSWLSLARVAHKKGELSMEDVWSLSK 138
 Db 24 RYDSLSKTMIPVRCARILAPRPVDAGLSFATSWLTPVWVKYRQ-RLVDTLPPLST 82
 QY 139 HESSDVNCRRLERLMOEBLNEVGPDAASLRNVVIFCRTLILSYICLMTITQLAGSGPA 198
 Db 83 YDSSDTNAKKRRVLMDEVARVGEKASLSHVWVKFQRTVIMDVNIICIIIMAAIGPT 142
 QY 199 FMVNHLEYQATSNLQYSLVILGLLPEIYVMSGLATWALNRYGVRLBAGAILTMA 258
 Db 143 VLIHQILOQERTSGKWWGIGLCTALFATEFTVFPMALAMAINYFARILKVALSTLV 202
 QY 259 FKKLIKNIKEKSGELINICSDGOMFEAAVGSLLAGGPVALLGMIYNIIGPT 318
 Db 203 FENLVSEKTLTHISVGEVLNLTSSDYSLEFEALFCPLPATIPILMWCAAYAFIIGPT 262
 QY 319 GFLGSAVFIIFYPAMMPASRLTAYFRKRCVAATDERVOKMNEVLTITKFIKIMYAVKAFS 378
 Db 263 ALIGISYVIFIPVQMPAKINSAFRRSAILVTDKRVQTMNEFLTCTIRLIKIMYAKESFT 322
 QY 379 OSVOKIREERERILEKAGYFOSITVGVAPIVVIVIASVVTESVHMTLGFEDLTAQAFTVVT 438
 Db 323 NTIODIRREERKLEKAGFVQSGNSALAPIVSTIAIVLTISCHILLRKLTAAPAFAFSVIA 382
 QY 439 VFNMTFALKVTPRSVVSLSASAVADVRFKSLFMEVEYHMKNNPASPBIKIEKNATLA 498
 Db 383 MFNNMKFSIALLPFSIKAMAEANVSLRMRKILLDKSPSYITQPEPBDVLLANATLT 442
 QY 499 WDSHSSIONSPLTPMKKDKRASRGKKEKRVOLQRTHOAVLAEOKGHLLDSDERS 558
 Db 443 WEH-----EASRKSTPKKLQKOKRHCLKORSEAYSERSPA-----KG-----ATG 484
 QY 559 PEEBEGKHILGHLRLOTHSIDLEIOEKLVGICGSVSGKTSLSAIIAGMTLEGS 618
 Db 485 PEEQSDS-----LKSVLHSISFVVRKGIIGICGVSGKSSLLAALGQOLQGV 536
 QY 619 IAIISGTAYVAQOAMILNATLRDNLIFGKEYDERYNSVLSCLRPDLALPSSDLEI 678
 Db 537 VAVNGTLAYVQOAMIFHGNVRNLIIFGEKDHQRYOHTYAVCGLOKDLNLPYGDLEI 596

Best Local Similarity	99.1%	Pred. No. 5,26-258;			
Matches 564;	Conservative	0;	Mismatches	5;	Indels 0; Gaps 0

QY	869	NGSTAFSTWMLSYTKOGSSNTYTRGNETSVSSQMDNPHMOYVASIALSAVAVLLIL	928
Db	1	NGSTAFSTWMLSYTKOGSSNTYTRGNETSVSSQMDNPHMOYVASIALSAVAVLLIL	60
QY	929	KAIRGVVFKGTLRASSRLHDELFRILRILSPMKFPDTPPTGRILIRRSKDMDEVRLPF	988
Db	61	KAIRGVVFKGTLRASSRLHDELFRILRILSPMKFPDTPPTGRILIRRSKDMDEVRLPF	120
QY	989	QAEFQIONVILVEFCVGMIAGVFPMEVLAVGDLVILFVSVLHIVSRVLIRELKRLDNTQS	1048
Db	121	QAEFQIONVILVEFCVGMIAGVFPMEVLAVGDLVILFVSVLHIVSRVLIRELKRLDNTQS	180
QY	1049	PFLSHITSSIQGLATTHAANKQOEFLLRQOELLDNOAPFELFTCAMRWLAVRDLISIA	1108
Db	181	PFLSHITSSIQGLATTHAANKQOEFLLRQOELLDNOAPFELFTCAMRWLAVRDLISIA	240
QY	1109	LITTTGIMVILMHGOIPRPYVAGIAISYAAVLGLFPQFTVRLASETEAFETSVERINHYIK	1168
Db	241	LITTTGIMVILMHGOIPRPYVAGIAISYAAVLGLFPQFTVRLASETEAFETSVERINHYIK	300
QY	1169	TLSEAPARIKNKAPSPDMPQEGEVTFFENAEMRYRENPLVLKVKVFTIKPKKIGIVGR	1228
Db	301	TLSEAPARIKNKAPSPDMPQEGEVTFFENAEMRYRENPLVLKVKVFTIKPKKIGIVGR	360
QY	1229	TGSKSSSLGMAFLRVLVLSGGCKRIDGVNISDIGLADLRSLSTIIPQPVLFSTVNSNL	1288
Db	361	TGSKSSSLGMAFLRVLVLSGGCKRIDGVNISDIGLADLRSLSTIIPQPVLFSTVNSNL	420
QY	1289	DPFNQVYEDQIMPALEERTHMKECIAOLPKLTSEVMENQDNFVSVEROLLCIARALLRHC	1348
Db	421	DPFNQVYEDQIMPALEERTHMKECIAOLPKLTSEVMENQDNFVSVEROLLCIARALLRHC	480
QY	1349	KILILDEATAMDETDLILQETIRERAFADCTMLTIAHRLHTVLGSDRIWVLAOGVVEF	1408
Db	481	KILILDEATAMDETDLILQETIRERAFADCTMLTIAHRLHTVLGSDRIWVLAOGVVEF	540
QY	1409	DTPSVLLSNDSSRFYAMFAAENKVAVKG	1437
Db	541	DTPSVLLSNDSSRFYAMFAAENKVAVKG	569

RESULT	12
US-09-760-483-464	
: Sequence 464, Application US/09760483	
: GENERAL INFORMATION:	
: APPLICANT: Rosen et al.	
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies	
: FILE REFERENCE: P0214	
: CURRENT APPLICATION NUMBER: US/09/760,483	
: PRIORITY FILING DATE: 2001-01-16	
: Prior application data removed - consult PALM or file wrapper	
: NUMBER OF SEQ. ID NOS: 856	
: SOFTWARE: PatentIn Ver. 2.0	
: SEQ ID NO 464	
: LENGTH: 569	
: TYPE: PRT	
: ORGANISM: Homo sapiens	
: FEATURE:	
: NAME/KEY: SITE	
: LOCATION: (243)	
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids	
: NAME/KEY: SITE	
: LOCATION: (244)	
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids	
: NAME/KEY: SITE	
: LOCATION: (250)	
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids	
: NAME/KEY: SITE	
: LOCATION: (437)	
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids	

US-09-760-483-464

Query Match	39.2%;	Score 2865;	DB 21;	Length 569;
Best Local Similarity	99.1%;	Pred. NO. 5.2e-258;		
Matches 564; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

OY	869	NVGSTASTMNLSTMVKOGSGNTTVA	RGNETSVDSDKPNPHOYASITATLSMAVMTL	928
Dd	1	NVGSTASTMNLSTMVKOGSGNTTVA	RGNETSVDSDKPNPHOYASITATLSMAVMTL	60
OY	929	KALNGVFVAGTLRASRLDELFRRLILSPMKFEDPTTGRI	LNRFSKDMDEVVRLPF	988
Dd	611	KALNGVFVAGTLRASRLDELFRRLILSPMKFEDPTTGRI	LNRFSKDMDEVVRLPF	120
OY	989	QAEKFIONVLFFCYGMLAGVPFWFLVAVGVLVILSVLHIVSRVLRELRKDINTQS	1048	
Dd	121	QAEKFIONVLFFCYGMLAGVPFWFLVAVGVLVILSVLHIVSRVLRELRKDINTQS	180	
OY	1049	PFLSHITSSIOGLATTIHAANKGEELHRVOELLDDNQAPFLFTCAMRLAVRDLISIA	1108	
Dd	181	PFLSHITSSIOGLATTIHAANKGEELHRVOELLDDNQAPFLFTCAMRLAVRDLISIA	240	
OY	1109	LITTTGMIATVMHGOLPPAYAGAISYAVALGTFPOETRLASETPARTSEVERINHYIK	1166	
Dd	241	LITTTGMIATVMHGOLPPAYAGAISYAVALGTFPOETRLASETPARTSEVERINHYIK	300	
OY	1169	TLSLEAPARIKNRAPSPDPMOECEVTFFENAKMYRENELPLVLYKKVSFTTKPEKIGIYGR	1228	
Dd	301	TLSLEAPARIKNRAPSPDPMOECEVTFFENAKMYRENELPLVLYKKVSFTTKPEKIGIYGR	360	
OY	1229	TGSCKSSLGMAFLRYVELSGCCIKIDGVRIISDIGLADLRKSIIIPDEPVLFSGTVRSNL	1288	
Dd	361	TGSCKSSLGMAFLRYVELSGCCIKIDGVRIISDIGLADLRKSIIIPDEPVLFSGTVRSNL	420	
OY	1289	DPEFOYEODIMWALEERTHKKECIAQLPKLSEVENENDNFSVEBOLLCTARALLRHIC	1348	
Dd	421	DPEFOYEODIMWALEERTHKKECIAQLPKLSEVENENDNFSVEBOLLCTARALLRHIC	480	
OY	1349	KILILDEATAMDETIDLLOETIRRAFDCTMLTAHRLHTVLSDRIIMVLAOGOVEEF	1408	
Dd	481	KILILDEATAMDETIDLLOETIRRAFDCTMLTAHRLHTVLSDRIIMVLAOGOVEEF	540	
OY	1409	DFPSVLLSNDSSRFYAFMPAAENKNAVKG	1437	
Dd	541	DFPSVLLSNDSSRFYAFMPAAENKNAVKG	569	
 RESULT 13 US-09-668-628-1 Sequence 1, Application US/09668628 GENERAL INFORMATION: APPLICANT: Krasnow, Randi E. TITLE OF INVENTION: APP-BINDING CASSETTE PROTEIN FILE REFERENCE: PC-0021 US CURRENT APPLICATION NUMBER: US/09/668,628 CURRENT FILING DATE: 2000-09-22 NUMBER OF SEQ ID NOS: 19 SOFTWARE: PERL Program SEQ ID NO 1 LENGTH: 1331 TYPE: PRP ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc.feature OTHER INFORMATION: Incyte ID No: 7481813CD1 US-09-668-628-1				

0y	99	HPVNDAGFSCMTFSSSLARVAHKKGELMEDWLSKSHESDVCNRRLRLEJN	158
Dd	33	YPLDNAGFSTLYSWLTPRL-MQSLRSRIDENTIPRLSHDASDKNORRLRMBEVS	91
0y	159	EVGRDASLRVWVIFCRTRLLISTVCMLTQOAGFSGPAFWYKILLEYTQATESNDYS	218
Dd	92	RGRIEKASVLLVMRFORTRIFEDALGICFCIASYAGFLTPILPKLLEFSEQDLNVNHG	151
0y	219	LLVLVLGILTPFVSNLSALTMALNMYTQVRLGALITLMAFKILKLNKRKISGELIN	278
Dd	152	VGLCFALFLSCVSLSFSSSWIINOTFARFPAWVSFEKELIOFKSVNHIITSGEYIS	211
0y	279	ICSDNGQMFEMFAAVGSLLAGGVPAVALIYVWVILIGPFGSGAVELTFYPAMAFASR	338
Dd	212	FFTGQVNVLFEGVCYGRVLVLTQASLVIGSISSEYFIIGTAFIALICLYLVRPLAVPMR	271
0y	339	LTAIFRRKCAVADDERVQKNEVLTGFKTKMTAMWKAFSOSYOKITREERILKAGYF	398
Dd	272	MAVKAQHTSEVSQDRIRVISEVLTGCIKLKMTWKEPRAKIIEDIRRRERKELCGVL	331
0y	399	QSIPIVGAIRVVIVASVTFESVHNHTGDFDLTAQAFVTVVTFNSMFAKLVPRFSKLS	458
Dd	332	QSLVSTLFTLPTVAIVWVILHTSLKLAAMASMASLMLSLSLVSFPYIAVKGP	391
0y	459	EASVAVDFKSLFMLEEVENHIKKRPA5PHIKIEMKNATIAMSSHSSISDKLTPKMK	518
Dd	392	NSKSAVMFKFFLQESBPVYUQTLDOPSKALVEEATILSMOQTCHGIVNG-----	442
0y	519	DKRASRGKKEVROLDTEHQAVALQCKHLLDSDBP-----SPEEDGKIIHLGHL	574
Dd	443	-----ALELENGH-ASEGMRTPDALGPRBEENS-----L	472
0y	575	QRTSHSIDLEIOEKGVLGICGVSQSGTSL5AILCOMTLEBSLISGTFPAVQAQAI	634
Dd	473	GPELHKINLVYKSKMMLGVCNGTSGKSLSL5ILEMHLBESVYUGSLAVYUQAMI	532
0y	635	LNATLRDNLIFGKEDEERYEYVNLNSCRLPDLALPPSSDLTEIGERGANLSGQORIS	694
Dd	533	VSGNIREMILMGAYDKARLYOVLHCCSLRDLELPRGDMTEIGERGLNSGQOKORIS	592
0y	655	LARALSPRSYLIIDDLPSALMDAHVGNFNSAIRKNL5KVLPTHOLOLDYDODEY	754
Dd	593	LARAVYSDROLYLIDDLPSAVDAHVGNHREB5ICKTKLTKKTVVLTHOLOLDYFCGQIT	652
0y	755	FMAEBCITERGTEHBLNMLNGDAVTFNNLLGERTPRVEIN5KKEYSQOKSODKGRPT	814
Dd	653	LLENGKICENTH5ELMOKKGAQOLIOKHNKREAT5DMLODPAKIAKRVESQALATSL	712
0y	815	GSIKKEKAVKREBQOLVLEKQGSVPM5VUVYIOAAGRLAFLVIMALEMNVG5TA	874
Dd	713	BESINGNAV--PEHQLOEEMEGESLSMRVUNHUYIOAAGVW5CITFFVLLVILFLLTI	770
0y	875	FSYMLNL5WIKQSGNTTVRGNMETS--DSMKDNHMOUYASIAL5MAVWLLIKALRG	933
Dd	771	FSPMNL5WLEQSGTSSREBSNCTMA5DL5NDNOL5FYQVLYGNALLICVGCYSS	830
0y	934	VVFKVGLTRASSRLHDELFRRLR5PKKFEPTTPGRILN5R5KDMDEV5VRLPQAEWF	993
Dd	831	GIFKTVTRKASTAHNKL5FKVFR5CPSFDITPIRGLN5CFAGDEOLEODOLL5PFSBOF	890
0y	994	IQNVILVEFCVM5AGFPMF5LAV5GRVL5LESVLAIV5RVL5RELKLRDNTQ5PPLSH	1055
Dd	891	LVL5LWIAVAVLIV5SPYLLMGALINIC5TYI5MFKKAL5GVKRL5ENT5K5P5L5H	950
0y	1054	ITTSIOGLATIHAVNKGQF5LHYOE5LD5NQAPFL5FCAM5KRLAV5RLD5L5ALITTT	1113
Dd	951	ILNSDGL5SIHYVKG5DEDFISO5FKRL5DQANN5YLL5FL5SRMVAL5RL5EINT5VLTAV	1010
0y	1114	GLMVLVNHGQIPRAYAGL5IA5VOLT5GL5FO5FVRL5L5E5ARF5SV5EKNIN5YIT5L5E	1173
Dd	1011	AL5PAFG5ST5P5F5K5MA5NIV5LO5L5ASS5Q5A5PAR5GL5TE5Q5FA5VER5I5LO5M5CV5E	1070

QY 1174 APARINKKAPSPWPOGEVTFENAEKRYRENPLVLKKSFTIKREKIGIVRTSGSK 1233
 Db 1071 APLHMGTSOPQPMQHGELIFQDYHMKYRDNPVYLAGINTLRGHEVVGIGRGSGK 1130
 QY 1234 SSIGMLFLVELSGGCIKIDGRISDIGLADRSKLSIIPBQVLESQVRSNLPDQ 1293
 Db 1131 SSIGMLFLVELSMAGRIIDVDICISIGIEDIRSKLSVLPDPVLLSGIRRLNDFDR 1190
 QY 1294 YTEDQIMDALERTHMECAIQLPLKLESEVWNGDNFVSEROLLCTARALLHCKLIL 1353
 Db 1191 HFDQIMDALERTFTLRKAIKSPKRLHTDVENGDNFVSEROLLCTARAVLRNSKILIL 1250
 QY 1354 DETAAMDPTDILLQETIREAFADCTMLTIAHRLHTVLSGDSRLMVAOCQVPEPTPSV 1413
 Db 1251 DEVTASIDMETDILLQRTIREAFQGTIVIAHRTVTLNCDRLVNGKGVVEEDREY 1310
 QY 1414 LLSNDSREYAFMAFAAENKY 1433
 Db 1311 LRKKPSLFAALMATATATSSL 1330

RESULT 14

US-09-703-253-18
 Sequence 18, Application US/09703253

GENERAL INFORMATION:
 APPLICANT: Harris, Marie
 APPLICANT: Donoho, Gregory
 APPLICANT: Turner, C. Alexander Jr.
 APPLICANT: Nehls, Michael
 APPLICANT: Friedrich, Glenn
 APPLICANT: Zambrowicz, Brian
 APPLICANT: Sands, Arthur T.
 TITLE OF INVENTION: Novel Human Transporter Proteins and
 TITLE OF INVENTION: Polynucleotides Encoding the Same
 FILE REFERENCE: LEX-0081-USA
 CURRENT APPLICATION NUMBER: US/09/703,253
 PRIOR FILING DATE: 2000-10-31
 PRIOR APPLICATION NUMBER: US 60/163,018
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 18
 LENGTH: 1379
 TYPE: PRN
 ORGANISM: homo sapiens
 US-09-703-253-18

Query Match 36.1%; Score 2637; DB 21; Length 1379;

Best Local Similarity 40.5%; Pred. No. 5.9e-236; Matches 552; Conservative 256; Mismatches 504; Indels 48; Gaps 8;

QY 77 PKGYHHGLALKPIRTTCKHQHVDNAGLFCSCWTFMSLSLAVARHKKGLSMDWLSL 136
 Db 60 PKGYHGLALKPIRTTCKHQHVDNAGLFCSCWTFMSLSLAVARHKKGLSMDWLSL 117
 QY 137 SKHSSDYVNCRLERLMOELINEVGPDAASLRVWIFCTRLILSVCLMITOLAGFSG 196
 Db 118 SVHSDAKNVOHRLHWEVEVSRGIRKASVILVLRPFRLLJEDALGICFIASVIG 177
 QY 197 PAFVAKLLLEYQTATNESLQYSLVLLGLLLETIVRSKSLATMALNRTGVRLGALT 256
 Db 178 PILIPIPLEYSEQLNVHVGVLCEFLALFLSECVKSLSFSSSWIINQRTAIRQAAVSS 237
 QY 257 MAEKKILKNIKIKSEGLINICSDNGQRMFEAAVAGSLAGPVAAILGMIVNIIIG 316
 Db 238 PAFKLLQFQSVHITTSGEALISFTGDVNYLFEGVCTGPLVLITCASLVTSISSYFIIIG 297
 QY 317 PTGLGSAVFLFYPAAMFASRLTAFFRRKCAATDERVQKMEVLYTIKIKYAWYKA 376
 Db 298 IYTAIATLCYLVLPLEFVFMRAVKAQHNSSEVSDORIRVTSLELNCIKIKYTWMEKP 357
 QY 377 FSGSVQKIRREERIRLEKAGYFOSITGVAVPIVVVIVSVTFVSHMILGFLTAQAFTV 436

QY 358 FAKIIEULRKRKKLEKGLVOSLSTITLPIYATFAFWLHNSKLKLAASNAFMS 417
 QY 437 VTFVNSMTFALKYTPSPVSKSLSEASVADRFKSLFLMEEVHMKIKNPASPHIIEKNAT 496
 Db 418 LASINLRLSVFPVPIAVKGLTNSKSAVMRRKFFLOESPVYVOTLQDSKALVEEAT 477
 QY 497 LAMDSHSSITQNSPKLTPKAKKDKRASRGKKVROQRORHQAVALAEOKGHLLQSDER 556
 Db 478 LSWQCTCPGIVNG-----ALIEIRNGH--ASEGMR 506
 QY P-----SPEEEGKHILGHLRLQRTLSIDLEIQGLVIGSGVSGKTSLSAIIQGM 612
 Db 507 PRDALGPEEBGNS-----LGPBLKILNVYSKGMMLVCQGTGSGKSSLSAILEM 558
 QY 613 TLEGSTAIGSTAYVAQAAMILNATLRDNLGKEYDEERYNSVLSCLRPDLALPS 672
 Db 559 HLEGSVQVQGLAYVPOQAMIVSGNIRENIMLGAVDKARYLOVLHCCSILNRDLLELP 618
 QY 673 SDLTEIGERGANLSSGORORISLARALYSRSTIYIILDDPLSALDAHGNHFNASIRKHL 732
 Db 619 GDMTEIGERGLNLSGGOKRISLARAVSDROYLDDPLSADAHGKHIFEECIKRTL 678
 QY 733 KSKTVLEFVTHQLOXYVDCDEVYEFMKEGCITERGTHEELMNLNGDYATIFNNLLGEPV 792
 Db 679 RGTIVLVTHQLOXYLEFCGQIILLENKICENGTHSLELMQKKYQADLOKMKHEATSDM 738
 QY 793 EINSKKESSQOKKSDOKPRTGSIKKEKAVKPEEGOLVLEEGGQSVSPVYGYTQA 852
 Db 739 LQDTAKIAERPKVESQALATLSLESLNGNAV--PEHOLTOEEEBEESLSRNVHNYQA 796
 QY 853 AGGPLAVLIVMALFMLNVGSAFSTWMLSWIKSGNVTYTRGNESVVS--DSKNDPMH 911
 Db 797 AGGTWAGCIIFFEVYLVLFILFESFMWLSWLEGGSGTNSRRENGTMADLGNATNDPOL 856
 QY 912 QYASIALSMAVAILKAIKRGVVFVVKATLRASSRLDELFRLIRSPMKFEDTTPGRI 971
 Db 857 SFYLVYGLNALLILICVGCSSGIFTKVTRKASALHNKLFKNKVERCPMSEFDIPIGLR 916
 QY 972 LNRFSKDMDEVDRLPQOAEKFIQNVILVFECVGMIAGVFPFVLVAVGPLVILFVSVAHV 1031
 Db 917 LNCFAGLDEQDOLPLTFSEQFLVLSLAVLIVSLVSPYILMLGAILWICFIYMM 976
 QY 1032 SRVLIRELKRDLNTGSPFISHINSIOGLATIHAIVKNGOELFRLHYOELDDNOAPFLF 1091
 Db 977 FKAIGVFKRLNYSRSLSHILNSLOGLSSHYGKTEFISQFKRLTDQANNYLLIF 1036
 QY 1092 TCAMRLAVRLDLISIALITTTGLMIVLMHGOIPPAYAGLAISYAVOLDTGLQFTVRLAS 1151
 Db 1037 LSTRWMLRLREIMTNLVTALVALFVAFGISSTPSYFVMAVNVILQASSFOATARIGL 1096
 QY 1152 ETEAFTSVERINHYIKTSLSEADPARIKKAPSPDWPOGEVTFENAEKRYRENPLVLK 1211
 Db 1097 ETEAFTSVERINHYIKTSLSEADPARIKKAPSPDWPOGEVTFENAEKRYRENPLVLK 1156
 QY 1212 KVSFTIKPKKIKIGVGRSGSSIGMALFRLVELSGGCIKIDGRISDIGLADRSKLS 1271
 Db 1157 GINTLRHEVVGIVGRSGSSIGMALFRLVELSMAGRIIDVDICISIGIEDIRSKLS 1216
 QY 1272 IIPQPVLESQVRSNLDPEQYTEDQIMDALERTHMECAIQLPLKLESEVWNGDNFVS 1331
 Db 1217 VIPQPVLESQVRSNLDPEQYTEDQIMDALERTHMECAIQLPLKLESEVWNGDNFVS 1276
 QY 1332 VGEROLCTIARALLRHCKLILDENTAAMDPTDILLQETIREAFADCTMLTIAHRLHTV 1391
 Db 1277 VGEROLCTIARAVLRNSKIILIDEATASIDMETDILLQRTIREAFQGTIVIAHRTV 1336
 QY 1392 LGSRLVLAOGVYVEPTPSVLLSNDSREYAFMAFAAENKY 1433
 Db 1337 LNCDHILVWNGKGVVEEDREYLRKKPSLFAALMATATATSSL 1378

RESULT 15

US-09-775-685-46
: Sequence 46, Application US/09775685
: GENERAL INFORMATION:
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Mathur, Brian
: APPLICANT: Wang, Xiomang
: APPLICANT: Abuin, Alejandro
: APPLICANT: Friedrich, Glenn
: APPLICANT: Zambrowicz, Brian
: APPLICANT: Sands, Arthur T.
: APPLICANT: Donoho, Gregory
: APPLICANT: Hilbun, Erin
: TITLE OF INVENTION: Novel Human Transporter Proteins and Polynucleotides Encoding the
: TITLE OF INVENTION: Same
: FILE REFERENCE: LEX-0128-USA
: CURRENT APPLICATION NUMBER: US/09/775, 685
: PRIOR FILING DATE: 2001-02-02
: PRIOR APPLICATION NUMBER: US 60/179, 973
: PRIOR FILING DATE: 2000-02-03
: PRIOR APPLICATION NUMBER: US 60/182, 422
: PRIOR FILING DATE: 2000-02-14
: NUMBER OF SEQ ID NOS: 71
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 46
: LENGTH: 1216
: TYPE: PRT
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (1)...(1216)
: OTHER INFORMATION: Xaa - Any Amino Acid
US-09-775-685-46

Query Match 35.4%; Score 2583.5; DB 21; Length 1216;
Best Local Similarity 43.6%; Pred. No. 4.8e-231;
Matches 535; Conservative 227; Mismatches 410; Indels 55; Gaps 13;

QY 80 KYHGLSLAKPRITTCQ-HQHPVDNAGLFCSCMTFSLSLAVAHKKGSLMEDVWSLSK 138
DB 24 RDPSPKTMIPKPCARLAPNPVDAGLSPATFSLTPVVMKGYRQ-RLTVDTLPLST 82
QY 139 HESSVNCRRLERLMOELENVGPDAASLRVYVIFCRRLILSYCLMIIQLAGSPGA 198
DB 83 YDSSTNAKRFVLMDEEVARVGPKEKASLSHYVWKFORRVLMIDYANILCIIMAIQPT 142
QY 199 FMVKHLEYQTATESNLQYSLLVGLLTETIVSRMSLALFWALYRFGVRLGAILTMA 258
DB 143 VLIHQILOQTERTSKVMWGICLIALFATEFTKYFFMALAMAINRTAIRLKVALLSTIV 202
QY 259 FRKIILKNIKESLIGELINCSNDGORMFEAAGSLAGSPVVAIIIGMIVNIIIGPT 318
DB 203 FENLVSFRTLHISVGEVLNLTSSDYSLSFEALPCPLPATPIIIMVFCAAVAFILGPT 262
QY 319 GLISAVFLEFPYAMFASRLTAYFRRCVATDEROVKNENVYIKFIKMYAMWKAS 378
DB 263 ALIGSVYVIFPVOMFAKLSAFRRRSAILVTDKRVOTMNEELTCIRLIKIMAMEKST 322
QY 379 OSVOKIREERRLIKAGYFOSITVGAPVIVVIVASVTVFSVMTLGFDTLTAQAFTVVT 438
DB 323 NTIODIRRRERKLKAGVSGNSALAPIVSTIAIVLISCHILLRKLTPAPVAFVIA 382
QY 439 VFNSTFPAKTYPFVSKISEASVAVDRKSLFLMEVHMINKKSPASPIKITEMKNATLA 498
DB 383 MENVKFSIALIPFSIKMAEAVNSLRMKKILIDKSPSYITOPEDPDTVILLANATLT 442
QY 499 WDSHSSSIONSPKLPKKMKRDRASRGKEKVRQLOQTEHOAVLAEQKGLLSDERS 558
DB 443 WEH-----EASRSTPKLQNKRLCKKORSEANSERPPA-----KG-----ATG 484
QY 559 PEEEGKHIHLGLRLQRTLSIDLEIOGKLVGICGVSQKTSLSAIILOQMTEGSS 618
DB 485 PEEGSDS-----LKSVLHSISFVVRKRGKITGICGNVSGKSSLLAALLOQMOLQKV 536

QY 619 IALSGFAVVAQOAMTLNLTIRNDILFGEKYEDEERNVLSNCCLRPDALILPSSDLTEI 678
DB 537 VAVNGTILAVSQAAMTEHNVRENILFGEKYHORQHTVVRVCGLOKDLSTNIPYGLTEI 596
QY 679 GERGANLSSGQORISLARALYSDRSITYLLDDPLSLADAHVGNHFNPSAIRKHLKSTVL 738
DB 597 GERGLNLSGQORISLARALYSDRSITYLLDDPLSLADAHVGNHFNPSAIRKHLKSTVL 656
QY 739 FVTHOLOLVDCDEVIFEMKEGCTTERGTHEELMNLNGDYATTFNNL-LIGETP----- 790
DB 657 LVTHQLOFLESCDEVILLDEGEICEKGTKEIMEERGRYAKLIHNLRGLOFQDEHLVNA 716
QY 791 -----PVEINSKKETSGSOKSODKPRGTGSIKKKAKAPREGOLVLEKGGGSV 841
DB 717 AMVEAFKESPARREDAVLAPGNEKDEKESSETGS--EVDVTKVPBHOLIQTESPDGTV 774
QY 842 PMSVYGVYIOAAGPLAFVIALFPLANGSTAFTSMVLSYNIKQSGNVTYTRGNET-- 899
DB 775 TTKTYHTTYIKASGGYLLSLFTVFLPLMIGSAFNMWLGMLDKGSRMTCCGPGNRTMC 834
QY 900 SVSDSKMD-NPHMOYVYASIALSMAYMLLKAIRGVVEYKGLRASSRLHDELFRRLRS 958
DB 835 EVGAVLADIGQHV--YQWVYASVMEVMEVGYTKGFVFTKTLTMASSSLHDFVFKILKS 892
QY 959 PMKFEDTPTTGRLNRFKSDMDQEDVRLPFOAMFQNIQNIYLFVFCYGMAGVFPMPVLAV 1018
DB 893 PMSFEDTPTTGRLNRFKSDMDQEDVRLPFOAMFQNIQNIYLFVFCYGMAGVFPMPVLAV 952
QY 1019 GPLVILFSLHIVSRVRLIRELRLDNIQSPFLSHITSSIOGLATIHAYNKGQEFLLRVQ 1078
DB 953 ASLAVGFILLKIFHRGVOELKKEVNSRSPMFTHTTSSMOGLIITHAIGKKEST---T 1009
QY 1079 ELDDNQAPFLEFPCAMRLAVRLDLISIALITTTGLMIVLMHGOIPPAVAGLAISYAVQ 1138
DB 1010 TINDENSHLVEFNCALRFALRMVLMNITFTVALLVTLSPSSISTSSKGLSISYIQ 1069
QY 1139 LGLQFOFYRLASEFARTSVERRINHXYKTLSTLEPAKIKKAPBDMPOBGEVFEENA 1198
DB 1070 LSGLLQVCVTRGTQAKTSVELLEXYISTVCVPECTHPLKVGTCRKPMPKSGEITFRDY 1129
QY 1199 EMKRYRENPLVLKRYVSTFKPREKIGIVGTSGKSSLMALFRLVELSGGCXIKIDGVR 1258
DB 1130 QMRKRYNDPTVLVDSLNLNIOGOTYGVRTSGKSSLMALFRLVEPASGITIFIDEVDI 1189
QY 1259 SDIGLADLRSKLSIIPQEPVLEFSGTVR 1285
DB 1190 CILSLEDLRTKLTVPIDQPVLEFVGTVR 1216

Search completed: August 11, 2002, 11:12:12
Job time: 6682 sec

